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OM protein - protein search, using sw model

Run on: October 30, 2002, 15:45:05 ; Search time 31 Seconds

(without alignments)
902.922 Million cell updates/sec

Title: US-09-910-033a-2

Perfect score: 1290

Sequence: 1 MSRLDGKVAITGTLGIG.....NESKATGSEFVVDGGYTAQ 252

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_032802:**
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:**
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:**
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:**
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9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:**
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:**
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:**
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:**
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:**
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:**
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:**
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:**
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19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:**
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:**
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:**
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1277	99.0	252	18 AAW23407	Lactobacillus brev
2	1019	79.0	251	18 AAW23409	Lactobacillus kefi
3	456	35.3	254	22 AAB49773	Protein with acety
4	450	34.9	254	22 AAB47522	(R)-2-octanol dehy
5	400	31.0	258	21 AAY56815	Bacillus D-arabini
6	369	28.6	272	22 AAU37095	Staphylococcus aur
7	367.5	28.5	261	13 AAR27757	Glucose dehydrogen
8	364.5	28.3	261	11 AAR04044	Glucose dehydrogen
9	364.5	28.3	261	13 AAR24018	Thermostable gluco
10	364	28.2	251	22 AAU34193	Staphylococcus aur
11	363.5	28.2	272	21 AAB10740	B. megaterium gluc

12	363.5	28.2	340	21 AAB10741	H. ghiliani/B. me
13	360.5	27.9	261	11 AAR03846	Modified glucose d
14	359.5	27.9	261	13 AAR27756	NAD affinity gluco
15	358.5	27.8	261	9 AAR80590	Sequence of glucos
16	358.5	27.8	261	21 AAY96271	B. subtilis glucos
17	358.5	27.8	261	21 AAY54424	Amino acid sequenc
18	356.5	27.6	261	9 AAR80063	Glucose dehydrogen
19	352.5	27.3	262	22 AAG83032	S. epidermidis ope
20	351	27.2	286	22 AAG36267	Pseudomonas aerugi
21	345	26.7	306	22 AAG81844	S. epidermidis ope
22	344	26.7	270	21 AAB42558	Human ORFX ORF2322
23	340	26.4	270	20 AAB41761	Human PRO474 (UNQ5
24	340	26.4	270	21 AAB44317	Human PRO474 (UNQ5
25	340	26.4	270	21 AAB24056	Human PRO474 prote
26	340	26.4	270	22 AAU28108	Novel human secret
27	340	26.4	279	22 AAU18296	Human endocrine po
28	336.5	26.1	271	22 AAU37794	Streptococcus pneu
29	336.5	26.1	272	22 AAU38086	Streptococcus pneu
30	334.5	25.9	288	22 AAU28296	Novel human secret
31	330.5	25.6	277	21 AAY54415	Secoisolaricresin
32	324	25.1	336	16 AAW06488	Maize T52 sequence
33	322	25.0	286	21 AAY92509	Human OXRE-6. Hom
34	319.5	24.8	256	17 AAW02111	Glucuronate:NADP+-5-
35	317.5	24.6	262	20 AAY08329	A. parasiticus ver
36	317.5	24.6	263	22 AAG81555	S. epidermidis ope
37	317	24.6	241	12 AAR10679	Acetoacetyl CoA re
38	317	24.6	300	21 AAG18820	Arabidopsis thalia
39	317	24.6	343	21 AAG18619	Arabidopsis thalia
40	316	24.5	248	21 AAY54422	Amino acid sequenc
41	314	24.3	283	21 AAG31552	Arabidopsis thalia
42	312.5	24.2	260	17 AAR94617	3-hydroxybutyric a
43	311.5	24.1	253	22 AAU36249	Pseudomonas aerugi
44	311.5	24.1	289	22 AAG83109	S. epidermidis ope
45	309.5	24.0	272	21 AAG09589	Arabidopsis thalia

ALIGNMENTS

RESULT 1

AAW23407

ID AAW23407 standard; Protein; 252 AA.

XX AAW23407;

XX DT 27-MAR-1998 (first entry).

XX DE Lactobacillus brevis alcohol dehydrogenase.

XX KW Alcohol dehydrogenase; production; (R)-alcohol; (S)-alcohol.

XX OS Lactobacillus brevis.

XX PN EP796914-A2.

XX PD 24-SEP-1997.

XX PF 20-MAR-1997; 97EP-0104814.

XX PR 21-MAR-1996; 96DE-4010984.

XX PA (BOEF) BOEHRINGER MANNHEIM GMBH.

XX PI Hummel W, Riebel B;

XX DR WPI; 1997-459831/43.

XX DR N-PSDB; AAT73132.

XX Lactobacillus brevis alcohol dehydrogenase - useful for production of optically active alcohol(s)

XX PS Claim 8; Pages 24-26; 34pp; German.

CC The present sequence is a Lactobacillus brevis alcohol
 CC dehydrogenase, which retains at least 95% of its activity after 30
 CC minutes at 20-60 degrees C and can be purified to a specific
 CC activity of at least 400 U/mg. The enzyme can be used to produce
 CC (R)-alcohols by enantioselective reduction of ketones of formula
 CC R1-CO-R2, where R1 and R2 = hydrogen (sic) or 1-20C alkyl, alkenyl,
 CC aryl or arylenyl (sic) optionally substituted by halogen, NO2, OH
 CC or 1-20C alkoxy, "an optionally substituted 1-10C alkylene group,
 CC which is substituted by saturated, unsaturated or aromatic
 CC nitrogen, oxygen or sulphur heterocycles, or may be an optionally
 CC substituted polycondensed saturated and/or aromatic group" (sic) in
 CC the presence of the enzyme or cells containing it at 20-60 degrees
 CC C for 0.25-3 hours, or (S)-alcohols by incubating a racemic alcohol
 CC of formula R1-CHOH-R2 in the presence of the enzyme or cells
 CC containing it at 20-60 degrees C for 0.25-3 hours.

XX Sequence 252 AA;

Query Match 99.08; Score 1277; DB 18; Length 252;
 Best Local Similarity 99.24; Pred. No. 6.5e-116;
 Matches 250; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSNRLDKVAIITGTLGIGLAIAATKFEVGEAKVMITDRHSDVGEKAASVGTDPDQIOFF 60
 DB 1 MSNRLDKVAIITGTLGIGLAIAATKFEVGEAKVMITDRHSDVGEKAASVGTDPDQIOFF 60
 QY 61 QHDSDEDEGWTKLDATEKAFGPVSTLVNNAGIAVNSVEETTTAEWRKLLAVNLGCVFF 120
 DB 61 QHDSDEDEGWTKLDATEKAFGPVSTLVNNAGIAVNSVEETTTAEWRKLLAVNLGCVFF 120
 QY 121 GTRIGIORMKNGKLGASTIINNKSSTEGFVGDPSLGAYNASKGAVRIMSKSAALDCKALDYD 180
 DB 121 GTRIGIORMKNGKLGASTIINNKSSTEGFVGDPSLGAYNASKGAVRIMSKSAALDCKALDYD 180
 QY 181 VRVNVHPGIKTPLVDDLPAGEAMSORTKTPMGHTGEPRNDIAYICVYLASNESKPTG 240
 DB 181 VRVNVHPGIKTPLVDDLPAGEAMSORTKTPMGHTGEPRNDIAYICVYLASNESKPTG 240
 QY 241 SEFVVDGCGYTAQ 252
 DB 241 SEFVVDGCGYTAQ 252

RESULT 2

AAW23409
 ID AAW23409 standard; Protein; 251 AA.

XX AAW23409;

DT 27-MAR-1998 (first entry)

XX Lactobacillus kefir alcohol dehydrogenase.

KW Alcohol dehydrogenase; production; (R)-alcohol; (S)-alcohol.

OS Lactobacillus kefir.

XX Key Location/Qualifiers

FT MISC-difference 46 /note= "not defined in specification"
 FT MISC-difference 47 /note= "not defined in specification"
 FT MISC-difference 48 /note= "not defined in specification"
 FT MISC-difference 49 /note= "not defined in specification"
 FT MISC-difference 50 /note= "not defined in specification"
 FT MISC-difference 51 /note= "not defined in specification"
 FT MISC-difference 52 /note= "not defined in specification"
 FT MISC-difference 53 /note= "not defined in specification"

FT MISC-difference 54 /note= "not defined in specification"
 FT MISC-difference 55 /note= "not defined in specification"
 FT MISC-difference 56 /note= "not defined in specification"
 FT MISC-difference 57 /note= "not defined in specification"
 FT MISC-difference 58 /note= "not defined in specification"
 FT MISC-difference 59 /note= "not defined in specification"
 FT MISC-difference 60 /note= "not defined in specification"
 FT MISC-difference 61 /note= "not defined in specification"
 FT MISC-difference 62 /note= "not defined in specification"
 FT MISC-difference 63 /note= "not defined in specification"
 FT MISC-difference 64 /note= "not defined in specification"
 FT MISC-difference 65 /note= "not defined in specification"
 FT MISC-difference 66 /note= "not defined in specification"
 FT MISC-difference 67 /note= "not defined in specification"
 FT MISC-difference 68 /note= "not defined in specification"
 FT MISC-difference 69 /note= "not defined in specification"
 FT MISC-difference 70 /note= "not defined in specification"
 FT MISC-difference 71 /note= "not defined in specification"
 FT MISC-difference 130 /note= "not defined in specification"
 FT MISC-difference 131 /note= "not defined in specification"

XX EP796914-A2.

XX 24-SEP-1997.

XX 20-MAR-1997; 97EP-0104814.

XX 21-MAR-1996; 96DE-4010984.

XX (BOEF) BOEHRINGER MANNHEIM GMBH.

XX Hummel W, Riebel B;

XX WPI; 1997-459831/43.

XX Lactobacillus brevis alcohol dehydrogenase - useful for production
 of optically active alcohol(s)

XX Example 8; Pages 28-30; 34pp; German.

XX The present Lactobacillus kefir alcohol dehydrogenase (ADH) was
 used in the isolation of a L. brevis ADH, which retains at least
 95% of its activity after 30 minutes at 20-60 degrees C and can be
 purified to a specific activity of at least 400 U/mg. The enzyme
 can be used to produce (R)-alcohols by enantioselective reduction
 of ketones of formula R1-CO-R2, where R1 and R2 = hydrogen (sic)
 or 1-20C alkyl, alkenyl, aryl or arylenyl (sic) optionally
 substituted by halogen, NO2, OH or 1-20C alkoxy, "an optionally
 substituted 1-10C alkylene group, which is substituted by
 saturated, unsaturated or aromatic nitrogen, oxygen or sulphur
 heterocycles, or may be an optionally substituted polycondensed
 saturated and/or aromatic group" (sic) in the presence of the

CC enzyme or cells containing it at 20-60 degrees C for 0.25-3 hours,
CC or (S)-alcohols by incubating a racemic alcohol of formula
CC R1-CHOH-R2 in the presence of the enzyme or cells containing it at
CC 20-60 degrees C for 0.25-3 hours.
XX
SQ Sequence 251 AA;

Query Match 79.0%; Score 1019; DB 18; Length 251;
Best Local Similarity 80.5%; Pred. No. 7.8e-91;
Matches 202; Conservative 14; Mismatches 35; Indels 0; Gaps 0;

QY 2 SNRLDGKVAITGGTIGLATATKFEVGEKAVMTDRHSDVGEKAASVGTDPDQIQFQ 61
DB 1 TDLRGKVAIVTGGTIGLATADAFVEGEKAVITGRHADVGEKXXXXXXXXXXXXX 60
QY 62 HDSDEDEGWTFLDATEKAFGVPSTLVNAGIAVNSVEETTAERKLLAVNLGCVFFG 121
DB 61 XXXXXXXXXXLFDATEEAFGPTTVNAGIAVNSVEDTTEERKLLSVNLGCVFFG 120
QY 122 TRLGQRMKNKGLGASIIINMSIEGFVDPSPGAYNASKGAVRIMSKSAALDCALKDYDV 181
DB 121 TRLGQAMKXXGLGASIIINMSIEGFVDPSPGAYNASKGAVRIMSKSAALDCALKDYDV 180
QY 182 RVNTHPGYIKTPLYDDLPGEAEMSORTKTPMGHIGEPNDIAYICVYLASHESKFATGS 241
DB 181 RVNTHPGYIKTPLYDDLPGEAEMSORTKTPMGHIGEPNDIAYICVYLASHESKFATGA 240
QY 242 EFVVDGGYTAQ 252
DB 241 EFVVDGGYTAQ 251

RESULT 3
AAB49773
ID AAB49773 standard; protein; 254 AA.
XX AAB49773;
AC AAB49773;
DT 23-APR-2001 (first entry)
DE Protein with acetylpyridine derivative reducing action.
KW Optically-active pyridineethanol derivative; asymmetric reduction.
XX Candida maris.
OS
PN WO200105996-A1.
XX
XX 25-JAN-2001.
XX
XX 28-JUN-2000; 2000WO-JP04237.
XX
XX 21-JUL-1999; 99JP-0206503.
XX
XX (KANF) KANEKA CORP.
XX
XX Kawano S, Horikawa M, Yasohara Y, Hasegawa J;
XX
XX WPI; 2001-159546/16.
DR N-PSDB; AAF29375; AAF29376.
XX
XX Efficient, high-yielding preparation of optically-active
PT pyridineethanol derivatives by stereoselectively reducing
PT acetylpyridine derivatives e.g. with enzyme having asymmetric reduction
PT activity, for pharmaceutical intermediates -
XX
XX Claim 14; Fig 1; 76pp; Japanese.
PS
CC This invention relates to a process for producing optically-active
CC pyridineethanol derivatives by stereoselectively reducing acetylpyridine
CC derivatives with an enzyme or enzyme source having asymmetric reduction
CC activity. The process is efficient and high yielding to give R and S
CC isomers by suitable manipulation. The method is for the preparation of

CC optically-active pyridineethanol derivatives by stereoselectively
CC reducing acetylpyridine derivatives, and also similarly for their
CC polycyclic analogues, for use as pharmaceutical and agrochemical
CC intermediates, as well as in fine chemical production. The present
CC sequence represents the amino acid sequence of the enzyme used in the
CC process which has acetylpyridine derivative reducing action.
XX
SQ Sequence 254 AA;

Query Match 35.3%; Score 456; DB 22; Length 254;
Best Local Similarity 40.2%; Pred. No. 4.1e-36;
Matches 104; Conservative 49; Mismatches 94; Indels 12; Gaps 5;

QY 1 MSNRLDGKVAITGGTIGLATATKFEVGEKAVMTD-----RHSVDYGEKAASVGTGP 54
DB 1 MSNFANKVLIIVTGLSGIGLAVAKKFLQGAARVTTISDISATEKYNTVVGEPRTEGIDVK 60
QY 55 DOIQFQHDSSDEDEGWTFLDATEKAFGVPSTLVNAGIAVNSVEETTAERKLLAVN 114
DB 61 N-VQYIQADASKEADNEKLISSETLSAFGLDLYVCANAGIATFTQTTDISYDVMRKVTSIN 119
QY 115 LDGVFFGTRGLGIQRMKNKGLGASIIINMSIEGFVDPSPGAYNASKGAVRIMSKSAALDC 174
DB 120 LDGVFMDKLAAYFLSKNKPAGIYVNGSIHSYVAAPGLSHYGAAGKGLLTQTMALEY 179
QY 175 ALKDYDVRVNTVHPGYIKTPLYDDLPGEAEMSQR-TKTPMGHIGEPNDIAYICVYLASN 233
DB 180 AAK--GIRVNSVNGYIKTPLYDDICP--KEHMDYLITQHPIGRLGRPEBIASAVAFCLSD 235
QY 234 ESKPATGSEFVVDGGYTAQ 252
DB 236 EATFINGISLLVDGGYTAR 254

RESULT 4
AAB47522
ID AAB47522 standard; Protein; 254 AA.
XX AAB47522;
AC AAB47522;
DT 04-DEC-2001 (first entry)
DE (R)-2-octanol dehydrogenase.
KW (R)-2-octanol dehydrogenase; ketone; alcohol; beta-NAD; co-enzyme;
KW oxidize; optical isomer; (R)-2-octanol; 4-haloacetate ester;
KW (S)-4-halo-3-hydroxybutyrate ester; HMG-CoA reductase inhibitor;
KW D-carnitine; (R)-propoxybenzene.
XX
XX Pichia finlandica.
XX
XX WO200161014-A1.
XX
XX 23-AUG-2001.
XX
XX 15-FEB-2001; 2001WO-JP01082.
XX
XX 16-FEB-2000; 2000JP-0043506.
XX 08-DEC-2000; 2000JP-0374593.
XX
XX (DAIL) DAICEL CHEM IND LTD.
XX
XX Kudoh M, Yamamoto H;
XX
XX WPI; 2001-596701/67.
DR N-PSDB; AAB43472.
XX
XX (R)-2-octanol dehydrogenase for producing intermediates for HMG-CoA
PT reductase inhibitors or D-carnitine -
XX
XX Claim 9; Page 83-85; 97pp; Japanese.
XX
XX This sequence represents (R)-2-octanol dehydrogenase which has the

following characteristics:

CC (1) produces ketones by oxidizing alcohol using beta-NAD as a
 CC co-enzyme; and produces alcohols by reducing ketones using beta-NADH
 CC as a co-enzyme; and
 CC (2) preferentially oxidizes the optical isomer (R)-2-octanol; and
 CC reduces 4-haloacetate ester to produce (S)-4-halo-3-
 CC hydroxybutyrate ester.
 CC (S)-4-halo-3-hydroxybutyrate esters are useful as intermediates
 CC for HMG-CoA reductase inhibitors or D-carnitine. (R)-propoxybenzene
 CC derivatives are particularly useful as intermediates for optical
 CC isomers of ofloxane (S)-(-)-9-fluoro-3-methyl-10-(4-methyl-1-
 CC piperazinyl)-7-oxo-2,3-dihydro-7H-pyrido(1,2,3-de)(1,4) benzoxadin-
 CC 6-carboxylic acid).

XX SQ Sequence 254 AA;
 Query Match 34.9%; Score 450; DB 22; Length 254;
 Best Local Similarity 39.0%; Pred. No. 1.6e-35;
 Matches 101; Conservative 46; Mismatches 100; Indels 12; Gaps 5;
 Qy 1 MSNRDLGKVAITGTLGIGLAIAATKFEVGEAKVMITD-----RHSDVGEKAASVGTG 54
 Db 1 MSYFNHKNVAVVTGALSGIGLSVAKKFLQLCAKVTISDVSGEKYKVTETVVALKAQNLNT- 59
 Qy 55 DOIQFFOHDSDEDEGWTKLPDATEKAGPVPSTLVNNAIAVNSVEETTTAEWRKLLAVN 114
 Db 60 DNLHYQADSSKEEDNKKLISETLATGGLDVCANAGIKGFAPTHETPFQVWKKVIAVN 119
 Qy 115 LDGVFFETRLGIQRMKNKGLGASINSSIEGFGDPSLGAYNASKGAVRTMKSAAALDC 174
 Db 120 LNVFLLDKLAINYWLEKSRPGVIVNMGVSHVFAAFLAHYGAAGKGVKLTOTLALAY 179
 Qy 175 ALKDYVRVNTVHPGYIKTPLVDLPQAEAEASQRTKT-PMGHIGEPNDIAYICVYLASN 233
 Db 180 A--SHGIRVNSVNPYISTPLIDEVP--KERLDKLVSLHPIGRLGRPEEVADAVFLCSQ 235
 Qy 234 ESKFATGSEFFVDDGYTAQ 252
 Db 236 EATFINGVSLPVDGGYTAQ 254

RESULT 5

AAV56815
 ID AAY56815 standard; Protein; 258 AA.

XX AC AAY56815;

XX DT 31-MAR-2000 (first entry)

XX DE Bacillus D-arabinitol dehydrogenase.

XX KW D-arabinitol dehydrogenase; clinical diagnosis; mycosis.

XX OS Bacillus sp.

XX PN JP11332569-A.

XX PD 07-DEC-1999.

XX PF 26-MAY-1998; 98JP-0143637.

XX PR 26-MAY-1998; 98JP-0143637.

XX PA (IKED-) IKEDA SHOKKEN KK.

XX PA (NIPK) NIPPON KAYAKU KK.

XX DR WPI; 2000-091353/08.

XX DR N-PSDB; AA246762, AA246763.

XX Arabinitol dehydrogenase gene encoding D-arabinitol dehydrogenase -
 PT useful as a clinical diagnosing agent for mycosis

XX PS Claim 1; Page 10-11; 14pp; Japanese.

XX

CC The invention relates to gene encoding D-arabinitol dehydrogenase,
 CC isolated from *Bacillus* sp. IKD-5A868 strain. The protein can be expressed
 CC by standard recombinant methodologies. D-arabinitol dehydrogenase is used
 CC as a clinical diagnosing agent for mycosis. The present sequence
 CC represents the D-arabinitol dehydrogenase enzyme.

XX SQ Sequence 258 AA;

Query Match 31.0%; Score 400; DB 21; Length 258;
 Best Local Similarity 39.4%; Pred. No. 1.2e-30;
 Matches 100; Conservative 41; Mismatches 101; Indels 12; Gaps 7;

Qy 4 RLDGKVAITGTLGIGLAIAATKFEVGEAKVMITDRHSDVGEKAA---KSVGTDPDQIOFF 60
 Db 8 RLDGRVITVTGAGLGRMALALAAQAGSHIVIRADRADEAQAENIRSCGV--EATV 65
 Qy 61 QHDSDEGWTKLPDATEKAFGPVSTLVNNAIAVNSVEETTTAEWRKLLAVNLDGVFF 120
 Db 66 QTDVTDEAQAVALIRQVEEQYGRDLVLVNNAGIVHKDRAELPYETWNRVNNVNLNVFL 125
 Qy 121 GTRLGIQRMKNKGLGASINSSIEG-FVGDPS-LGAYNASKGAVRIMSKSAALDCALKO 178
 Db 126 MSAAGKVMIRQSGK-SIINISSMSGLIVNTPQPAAYNVSKAGVIMLTSLASEWA--P 182
 Qy 179 YDVRVNTVHPGYIKTPLVDD--LPGAEEAMSQRTKTPMGHIGEPNDIAYICVYLASNESK 236
 Db 183 HGVVNTIAGYMKTKTEPYFAAGGEMIDKWLANTPMGRPGVPHELGGIAYILASOASS 242
 Qy 237 FATGSEFFVDDGYT 250
 Db 243 FATGGVETIDGYT 256

RESULT 6

AAU37095
 ID AAU37095 standard; Protein; 272 AA.

XX AC AAU37095;

XX DT 14-FEB-2002 (first entry)

XX DE *Staphylococcus aureus* cellular proliferation protein #1265.

XX KW Antisense; prokaryotic cellular proliferation protein;

XX KW antibiotic; antibacterial; drug design.

XX OS *Staphylococcus aureus*.

XX PN WO200170955-A2.

XX PD 27-SEP-2001.

XX PF 21-MAR-2001; 2001WO-0509180.

XX PR 21-MAR-2000; 2000US-191078P.

XX PR 23-MAY-2000; 2000US-206848P.

XX PR 26-MAY-2000; 2000US-207727P.

XX PR 23-OCT-2000; 2000US-242578P.

XX PR 27-NOV-2000; 2000US-253625P.

XX PR 22-DEC-2000; 2000US-257931P.

XX PR 16-FEB-2001; 2001US-269308P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Haselbeck R, Ohlsen KL, zyskind JW, Wall D, Trawick JD, Carr GJ;

XX PI Yamamoto RT, Xu HH;

XX DR WPI; 2001-611495/70.

XX DR N-PSDB; AAS54954.

XX New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -

XX PS Example 3; Seq ID No 12688; 511pp; English.
XX CC The invention relates to antisense inhibitors of genes essential to
XX CC prokaryotic cellular proliferation, their use in identifying the
XX CC genes, their use in the discovery of novel antibiotics, the essential
XX CC genes themselves and the encoded proteins. The prokaryotes used are
XX CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
XX CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
XX CC invention is also useful for the identification of potential new targets
XX CC for antibiotic development. The antisense nucleic acids can also be used
XX CC to identify proteins used in proliferation, to express these proteins,
XX CC and to obtain antibodies capable of binding to the expressed proteins.
XX CC The proteins can be used to screen compounds in rational drug discovery
XX CC programmes. The antisense nucleic acid sequence is also useful to screen
XX CC for homologous nucleic acids which are required for cell proliferation in
XX CC a wide variety of organisms. The present sequence represents an
XX CC essential prokaryotic cellular proliferation protein.
XX CC Note: The sequence data for this patent did not form part
XX CC of the printed specification, but was obtained in electronic
XX CC format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 272 AA;

Query Match 28.6%; Score 369; DB 22; Length 272;
Best Local Similarity 35.8%; Pred. No. 1.3e-27;
Matches 92; Conservative 42; Mismatches 109; Indels 14; Gaps 6;
QY 4 RLDGKVAITGTLGIGLAIAIKFVEEGAKYMITDRHSDVGEKAASVGTDPDQIOFFQHD 63
DB 3 RLENKVAIVTGSTGIGQASATAQAQAYLAVDAEAVSETVDKIKNSGDKAKAYVD 62
QY 64 SDEDEGWTKLFDATKAFGPVSTLVNNAGI--AVNKSVEETTTAEWRKILAVNLDGVFFG 121
DB 63 INAEQIDNFASEIREQFGHVDVLENNAGVDNAAGR--THEYPTDYDKIMVDMRGTFM 121
QY 122 TRLGTRMKNKGLGASINMSIEGFGDPSLGAYNASKGAVRIMSKAALDKALDYDV 181
DB 122 TKMLPLAMTK--GGSIVNTSFSGQAADLYRSYNAAGAVINFTKSIATYEG-RD-GI 177
QY 182 RVNTHVPGYIKTPVLDLPGAE-----AMSQRTKPMGHGEPNDIAICVYLASNE 234
DB 178 RANATAPGTIETPLVDKLTGTSEDEKGAFRNQKMTPLGLRGPPEVGLVWFLASDE 237
QY 235 SKFATGSEFVVDGYTA 251
DB 238 SSFITEIRIDGGYMA 254

RESULT 7
AAR27757
ID AAR27757 standard; protein; 261 AA.
AC AAR27757;
DT 11-MAR-1993 (first entry)
DE Glucose dehydrogenase.
KW GDH; mutant; recombinant; mass production; tetramer; thermostable.
OS Bacillus megaterium.
PH Key Location/Qualifiers
FT Misc-difference 96 /note= "site of Glu->Val or Lys mutation"
FT Misc-difference 252 /note= "site of Gln->Leu mutation"
FT Misc-difference 253 /note= "site of Tyr->Glu mutation"
FT Misc-difference 22 /label= Ser, Ala

FT Misc-difference 43 /label= Asp, Glu
FT Misc-difference 79 /label= Ala, Ser
FT Misc-difference 95 /label= Leu, Met
XX JP04258293-A.
XX 14-SEP-1992.
XX 13-FEB-1991; 91JP-0106927.
XX 13-FEB-1991; 91JP-0106927.
XX (AWAN) AMANO PHARM KK.
XX WPI; 1992-354684/43.
XX Glucose dehydrogenase preph. using transformed recombinant DNA
XX from Bacillus megaterium - has specified transformations giving
XX glucose dehydrogenase-expressing vector, introduced into E.coli.
XX for culture
XX Claim 1; Page 8; 12pp; Japanese.
XX The glucose dehydrogenase enzyme is encoded by a recombinant DNA
XX clone from Bacillus megaterium. The DNA sequence may be mutated by
XX site directed mutagenesis to introduce mutations to the protein
XX sequence (see feature table). The DNA may be used to transform E.
XX coli cells, and transformants may be cultured to mass produce GDH.
XX The mutant GDH is not influenced by ion strength, exists as a
XX tetramer and is thermostable.
XX Sequence 261 AA;
XX Query Match 28.5%; Score 367.5; DB 13; Length 261;
XX Best Local Similarity 33.3%; Pred. No. 1.7e-27;
XX Matches 85; Conservative 49; Mismatches 112; Indels 9; Gaps 4;
QY 1 MSNRDLGKVAITGTLGIGLAIAIKFVEEGAKYMITDRHSDVGEKAA----KSVGTDPQ 56
DB 1 MYKLEGKVVITGSGTGLGKXMAIRFATEKAKVYVNVYRSKEXEANSVLEEIKKVG--GE 58
QY 57 IOFFQHDSDGWTKLFDATKAFGPVSTLVNNAGIANKSVETTTAEWRKLLAVNLD 116
DB 59 AIATKGDVTVESDVINLVQSKIKEFGKLDVMINNAGXENPVSSHMSLSDNKVIDTNLT 118
QY 117 GVFFCTRLGIQRMKNKGLGASINMSIEGFGDPSLGAYNASKGAVRIMSKAALDCAL 176
DB 119 GAFLGSRKAIKVFVENDIKGTVINNMSVHEKIPTPLFVHYAASKGKMLTETLALEYAP 178
QY 177 KDYDVRVNVTHPGYIKTPVLDLPGAEAMSQRTKPMGHGEPNDIAICVYLASNES 235
DB 179 K--GIRVNNIGFGAINTPTINAEKFADPEQADRVESMIPMGYIGEPEETAATAVAALASSE 236
QY 236 KFATGSEFVVDGYT 250
DB 237 SYVTGTLFDGGMW 251
RESULT 8
AAR04044
ID AAR04044 standard; protein; 261 AA.
XX AAR04044;
XX 02-MAR-1993 (first entry)
XX Glucose dehydrogenase.
XX GDH; vector; E. coli; enzyme; assay; food.

```

OS  Bacillus megaterium.
XX
FH  Key      Location/Qualifiers
FT  Misc-difference 22      /label= SER, ALA
FT  Misc-difference 43      /label= ASP, GLU
FT  Misc-difference 79      /label= ALA, SER
FT  Misc-difference 95      /label= LEU, MET
XX
PN  JP02072878-A.
XX
PD  13-MAR-1990.
XX
PP  06-SEP-1988; 88JP-0223343.
XX
PR  06-SEP-1988; 88JP-0223343.
XX
PA  (AMAN ) AMANO PHARM KK.
XX
DR  WPI; 1990-121044/16.
XX
XX  Glucose dehydrogenase prodn. from Bacillus megaterium - by
PT  culturing recombinant DNA-contg. transformants in nutrient
PT  culture medium, used in food industry
XX
PS  Claim 1; ; 12pp; Japanese.
XX
CC  DNA encoding glucose dehydrogenase (GDH) derived from B. megaterium
CC  encodes the amino acid sequence below. The DNA may be integrated
CC  into a vector for replication in E. coli. A large amt. of GDH may
CC  be produced at low cost. The GDH is used in clinical laboratory
CC  tests in the food industry in enzymic assays for glucose
CC  determination.
XX
SQ  Sequence 261 AA;

      Query Match      28.3%; Score 364.5; DB 11; Length 261;
      Best Local Similarity 33.3%; Pred. No. 3.4e-27;
      Matches 85; Conservative 49; Mismatches 112; Indels 9; Gaps 4;

QY  1 MSNRLDGKVAITGGTGLGIGLAITATKVEEGAKVMTDRHSDVGEKAA----KSVGTPDQ 56
DB  1 MYKDLGKVVVITGSGTGLGKXMAIRFATEKAKVVVYRSKEXEANSVLEEIKVKG--GE 58
QY  57 IQFFOHDSSDEGWTKLFDATKAFGCPVSTLVNNAGIANKSVSEETTTAEWRKLLAVNLD 116
DB  59 ATAVKGDVTVESDVINLVOSIKIEFGKLDVIMINNAGXENPVSSHENSLSDWNKVIDTNLT 118
QY  117 GVFFGTRFLGTQRMKNKGLGASINMSIEGFGDPSLGAYNASKGAVRTMKSAAALDCAL 176
DB  119 GAFLSREAIKVFVENDIGTVINMSVHEKIPWPLFVHAASKGGMKLTETLALEYAP 178
QY  177 KYDVRVNTVHPGYIKTPL-VDDLPGAEAMSORTKTPMGHIGEPNDIAYICVYLASNES 235
DB  179 K-GIRVNNIGPGAINTPINAEKADPQERADVESHIPGYIGEPEIAVAANWLASSEA 236
QY  236 KTAGSEFVVDGGYT 250
DB  237 SYVTGITLFDAGGMT 251

RESULT 9
AAR24018
ID  AAR24018 standard; Protein; 261 AA.
XX
AC  AAR24018;
XX
DT  27-NOV-1992 (first entry)
XX
DE  Thermostable glucose dehydrogenase from Bacillus megaterium.

Thermostable; increased heat stability; GDH.
Bacillus megaterium.
Key      Location/Qualifiers
Misc-difference 22      /label= Ser, Ala
Misc-difference 43      /label= Asp, Glu
Misc-difference 79      /label= Ala, Ser
Misc-difference 95      /label= Leu, Met
/note= "together with residues 252,253 may be replaced by a thermostability-conferring amino acid provided that taken together they are not Glu, Gln, and Tyr respectively"
Misc-difference 252      /note= "together with residues 96,253 may be replaced by a thermostability-conferring amino acid provided that taken together they are not Glu, Gln, and Tyr respectively"
Misc-difference 253      /note= "together with residues 96,252 may be replaced by a thermostability-conferring amino acid provided that taken together they are not Glu, Gln, and Tyr respectively"
US5114853-A.
19-MAY-1992.
22-SEP-1989; 89US-0410844.
22-SEP-1988; 88JP-0237699.
(AMAN ) AMANO PHARM KK.
Makino Y, Negoro S, Okada H, Urabe I;
WPI; 1992-192176/23.
DNA contg. glucose dehydrogenase gene of Bacillus megaterium -
used to express heat stable protein in Escherichia coli, e.g. with
glutamine 96 replaced by alanine
Claim 1; Column 13; 10pp; English.
A DNA library was prepared in E. coli C600, and screened with probe
AAQ29704, resulting in 3 positive colonies. These were cultured, and
plasmid DNA prepared from them and cut with EcoRI and SalI. The
probe AAQ29704 was then used to probe a PAGE gel and found to
strongly hybridise with a 3.6kb fragment. The 3 colonies were all
thus found to have the same plasmid, and this was named pGDAL. pGDAL
was cut with EcoRI and Sau3AI, and a 930bp fragment produced and
sequenced, and was found to encode the sequence given. pGDAL was
then cut with EcoRI and PvuII and a 1.5kb fragment isolated. This
was then cloned into expression vector pKK223-3 and transformed into
E. coli JM105.
SQ  Sequence 261 AA;

      Query Match      28.3%; Score 364.5; DB 13; Length 261;
      Best Local Similarity 33.3%; Pred. No. 3.4e-27;
      Matches 85; Conservative 49; Mismatches 112; Indels 9; Gaps 4;

QY  1 MSNRLDGKVAITGGTGLGIGLAITATKVEEGAKVMTDRHSDVGEKAA----KSVGTPDQ 56
DB  1 MYKDLGKVVVITGSGTGLGKXMAIRFATEKAKVVVYRSKEXEANSVLEEIKVKG--GE 58
QY  57 IQFFOHDSSDEGWTKLFDATKAFGCPVSTLVNNAGIANKSVSEETTTAEWRKLLAVNLD 116

```

Db 59 ATAVKGDVTVESVNLVOSXIKFEKGLDMNNAKXENPVSSHESLSDMKNKVIDNTLT 118
QY 117 GVFFCTRLGIORMKNGKLGASIIINSSIEGFVCDPSLGAYNASKGAVRIMSKSAALDCAL 176
Db 119 GAFLGSREAIKVFVENDIKGTVINSSVHEKIPWPLFVHYAASKGKMLTETLALEYAP 178
QY 177 KOYDVVNVTVHPGYIKTPL-VDDLPGAEEAMSORTKTPMGHIGEPNDIAIYICVYLASNES 235
Db 179 K-GIRVNNIGGCAINTPINAEEKFADQBERADVESIMPYIGEPEIEIAAVALASSEA 236
QY 236 KEATGSEFVVDGGYT 250
Db 237 SYVTGITLEADGGMT 251

RESULT 10
AAU34193
ID AAU34193 standard; Protein; 251 AA.
XX AAU34193;
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #469.
XX
KW Antisense; prokaryotic cellular proliferation protein;
KW antibiotic; antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PP 21-MAR-2001; 2001WO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
DR N-PSDB; AAS52052.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
FS Example 3; Seq ID No 5689; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 251 AA;

Query Match 28.2%; Score 364; DB 22; Length 251;
Best Local Similarity 35.5%; Pred. No. 3 6e-27;
Matches 91; Conservative 42; Mismatches 109; Indels 14; Gaps 6;

QY 5 LDGKVAITGGTGLGIGAIATKFEVGEAKVMTDRHSVDYGEKAASVGTDPDQIOFFQHDS 64
Db 1 LENKVAVTGASTGIGQASAIALAOEGAYVLAVDIAEAVSETVDKIKNSDKAKAVVDI 60
QY 65 SDEGWTKLFDATKAFGVPVSTLVNNAGI--AVNKSVEETTTAEWRKLLAYNLGDGVFFGT 122
Db 61 ASEQQIDNFASEIREOFQGHVDVLFNAGYDVAAGR-IHEYPTDVKIKNNVDMRGTFMT 119
QY 123 RLGIQRMKNKGLGASIIINSSIEGFVCDPSLGAYNASKGAVRIMSKSAALDCALKDQYDR 182
Db 120 KMLPLMWTK--GGSIWNTSFSGQAADLYRSGYNAKAGAVINFTKISIAIEYG-RD-GIR 175
QY 183 VNTVHPGYIKTPLVDDLPGAEE-----AMSORTKTPMGHIGEPNDIAIYICVYLASNES 235
Db 176 ANAIAPGTIETPLVDKLTGCTSEDKEGKAPRENQKWTPLGLRGKPEVGKLVVFLASDES 235
QY 236 KEATGSEFVVDGGYTA 251
Db 236 SEITGETIRIDGGVMA 251

RESULT 11
AAB10740
ID AAB10740 standard; Protein; 272 AA.
XX
AC AAB10740;
XX
DT 26-JAN-2001 (first entry)
XX
DE B. megaterium glucose dehydrogenase GlcDH protein.
XX
KW Glucose dehydrogenase; GlcDH; fusion protein; detection.
XX
OS Bacillus megaterium.
XX
PN WO200049039-A2.
XX
PD 24-AUG-2000.
XX
PP 08-FEB-2000; 2000WO-EP00978.
XX
PR 19-FEB-1999; 99DE-1006920.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Linxweiler W, Burger C, Poeschke O, Hofmann U, Wolf A;
XX
DR WPI; 2000-558290/51.
DR N-PSDB; AAA97948.
XX
PT Glucose dehydrogenase fusion proteins, useful in expression systems for
PT quick detection of foreign proteins by gel electrophoresis -
XX
FS Disclosure; Page 54-55; 63pp; German.
XX
CC This invention describes a novel recombinant fusion protein (A)
CC comprising at least a first and a second amino acid sequence,
CC characterized in that the first sequence has the biological activity of
CC a glucose dehydrogenase. Glucose dehydrogenase is useful as a detector
CC protein (in a detection system) for any type of recombinant
CC protein/polypeptide in a fusion protein. Glucose dehydrogenase can be
CC used to detect protein-protein interactions, where it corresponds to a

CC partner of a recombinant protein/polypeptide. Expression vectors encoding
 CC the fusion proteins are useful to optimize the expression of the
 CC recombinant protein/polypeptide in a recombinant production method. The
 CC host cell is also useful for recombinant production of the
 CC protein/polypeptide. The fusion proteins containing glucose dehydrogenase
 CC can be quickly detected in SDS-PAGE gels. This sequence represents the
 CC Bacillus megaterium glucose dehydrogenase GlcDH which is used in the
 CC construction of fusion proteins as described in the method of the
 CC invention.
 XX
 SQ Sequence 272 AA;

Query Match 28.2%; Score 363.5; DB 21; Length 272;
 Best Local Similarity 31.5%; Pred. No. 4.5e-27;
 Matches 82; Conservative 51; Mismatches 108; Indels 19; Gaps 4;
 QY 1 MSNRLDGKVAITGTLGIGLAIAIKFVEEGAKVMIT-----DRHSDVGEKAASV 51
 DB 1 MYTDLKRVVITGSGTGLGRAMAVRFGQEEAKVYINYNNEEALDAKKEVEEAGGQAI 60
 QY 52 GTPDQIOFFQHDSDDEGWTKLDATEKAFGPVSTLVNNAIGIANKSVETTTAEWRKLL 111
 DB 61 -----IVQGDVTKEDVNLVQTAKFETGLDVMINNAAGVENPVPSHLSLONWNVKI 113
 QY 112 AVNLDGVFFGTRIGLQRMKNKGLGASIIINSSIEGFVDPDPSLGAYNASKGAVRIMSKSAA 171
 DB 114 DTNLTGAFGLSREAIKVFENDIKGNVINSSVHEMIPWLFVHYAASKGKMLTETLA 173
 QY 172 LDCALKDYDVRVNTVHPGYIKTPL-VDDLPAGEEAMSORTKTPMGHIGEPNDIAYICVYL 230
 DB 174 LEYAPK--GIRVNNIGPGAMNTPINAEKFADPEQRADVESMIPMGYIGKPEEVAVAFL 231
 QY 231 ASNESKATGSEFVVDDGYT 250
 DB 232 ASSQASVTGTITLFDGGMT 251

RESULT 12

AA10741
 ID AAB10741 standard; Protein; 340 AA.

AA10741;

26-JAN-2001 (first entry)

H. ghillani/B. megaterium fusion protein Tridegin/GlcDH.

Glucose dehydrogenase; GlcDH; fusion protein; detection; tridegin.

Heamenteria ghillani.
 Bacillus megaterium.

Key	Location/Qualifiers
Protein	1..68
Protein	/note- "tridegin protein"
	69..340
	/note- "GlcDH"

W0200049039-A2.

24-AUG-2000.

08-FEB-2000; 2000WO-EP00978.

19-FEB-1999; 99DE-1006920.

(MERE) MERCK PATENT GMBH.

Linxweiler W, Burger C, Poeschke O, Hofmann U, Wolf A;

WPI: 2000-558290/51.

N-PSDB; AAA97949.

PT Glucose dehydrogenase fusion proteins, useful in expression systems for
 PT quick detection of foreign proteins by gel electrophoresis
 XX
 XX Disclosure; Page 59-60; 63pp; German.

CC This invention describes a novel recombinant fusion protein (A)
 CC comprising at least a first and a second amino acid sequence,
 CC characterized in that the first sequence has the biological activity of
 CC a glucose dehydrogenase. Glucose dehydrogenase is useful as a detector
 CC protein (in a detection system) for any type of recombinant
 CC protein/polypeptide in a fusion protein. Glucose dehydrogenase can be
 CC used to detect protein-protein interactions, where it corresponds to a
 CC partner of a recombinant protein/polypeptide. Expression vectors encoding
 CC the fusion proteins are useful to optimize the expression of the
 CC recombinant protein/polypeptide in a recombinant production method. The
 CC host cell is also useful for recombinant production of the
 CC protein/polypeptide. The fusion proteins containing glucose dehydrogenase
 CC can be quickly detected in SDS-PAGE gels. This sequence represents a
 CC fusion protein constructed from the H. ghillani tridegin protein and the
 CC Bacillus megaterium glucose dehydrogenase GlcDH which is described in the
 CC method of the invention.

XX Sequence 340 AA;

Query Match 28.2%; Score 363.5; DB 21; Length 340;
 Best Local Similarity 31.5%; Pred. No. 6.1e-27;
 Matches 82; Conservative 51; Mismatches 108; Indels 19; Gaps 4;

QY 1 MSNRLDGKVAITGTLGIGLAIAIKFVEEGAKVMIT-----DRHSDVGEKAASV 51

DB 69 MYTDLKRVVITGSGTGLGRAMAVRFGQEEAKVYINYNNEEALDAKKEVEEAGGQAI 128

QY 52 GTPDQIOFFQHDSDDEGWTKLDATEKAFGPVSTLVNNAIGIANKSVETTTAEWRKLL 111

DB 129 -----IVQGDVTKEDVNLVQTAKFETGLDVMINNAAGVENPVPSHLSLONWNVKI 181

QY 112 AVNLDGVFFGTRIGLQRMKNKGLGASIIINSSIEGFVDPDPSLGAYNASKGAVRIMSKSAA 171

DB 182 DTNLTGAFGLSREAIKVFENDIKGNVINSSVHEMIPWLFVHYAASKGKMLTETLA 241

QY 172 LDCALKDYDVRVNTVHPGYIKTPL-VDDLPAGEEAMSORTKTPMGHIGEPNDIAYICVYL 230

DB 242 LEYAPK--GIRVNNIGPGAMNTPINAEKFADPEQRADVESMIPMGYIGKPEEVAVAFL 299

QY 231 ASNESKATGSEFVVDDGYT 250

DB 300 ASSQASVTGTITLFDGGMT 319

RESULT 13

AA03846
 ID AAR03846 standard; protein; 261 AA.

AA03846;

09-AUG-1990 (first entry)

Modified glucose dehydrogenase gene of Bacillus megaterium.

Glucose dehydrogenase; Bacillus megaterium; heat stability;
 glucose assay; ss.

Bacillus megaterium.

DE3931716-A.

29-SEP-1988.

22-SEP-1989; 89DE-3931716.

22-SEP-1988; 88JP-0237699.

(AWAN) AMANO PHARM KK.


```
XX PI Makino YS, Negoro S, Urabe IA, Okada HT;
XX DR WPI; 1990-100507/14.
XX XX
XX PT New DNA encoding modified forms of glucose dehydrogenase -
XX PT from Bacillus megaterium, having specific amino acid
XX PT replacements, with higher heat stability.
XX PS Claim 1; Page 13; 16pp; German.
XX CC The normal Glu-96 residue is replaced by Lys, Gly or Ala.Gln-252 by
XX CC Leu or Tyr-253 by Cys. Ser-22 residue can also be Ala, Asp-43 can be
XX CC Glu, Ala-79 can be Ser and Leu-95 can be Met.E.coli containing this
XX CC sequence will produce a form of GDH with improved heat stability. the
XX CC enzymes are useful for glucose assay and can be produced at low costs
XX CC or in large amounts.
XX CC See also AAQ03772.
XX XX
XX SQ Sequence 261 AA;
Query Match 27.9%; Score 360.5; DB 11; Length 261;
Best Local Similarity 33.6%; Pred. No. 8.2e-27;
Matches 86; Conservative 49; Mismatches 110; Indels 11; Gaps 4;
QY 1 MSNRLDGKVAITGGTGLGIGLAIAATKFEVEGAKVMT-----DRHSDVGEKAASVGTDP 55
DB 1 MYKDLGKVVVITGGSTGLGKSMARFATEKAKVVVYRSKEDANSVLEEIKKVGGEAI 60
QY 56 QIQFOHSDSDGDKTKLFDATKAFGPVSTLVNAGIAVNSKVSVEETTTAEWRKLL 115
DB 61 AV---KGDVTVESDVNLVQSAIKFEGKLDVMINNAGLNXPVSSHMSLSDNKVIDTNL 117
QY 116 DGVFFTRIGIORMKNGKLGASIIINSSIEGFGVDPGLGAYNASKGAVRIMSKSAALDCA 175
DB 118 WGAFLGSRRAIKFYFVENDIKGVINSSVHEKIPWFLFVHYAASKGKMLMHWLALAYA 177
QY 176 LKDYDVRVTVHPGYIKTPL-VDDLPGAEEAMSQRTKTPMGHIGEPNDIAYICVILASNE 234
DB 178 PK--GIRVNNIGPGAINTPINAKEFPADPQERADVESMIPMGYIGEPEETAAVAANLASSE 235
QY 235 SKFATGSEFVVDGGYT 250
DB 236 ASVTGCTITLFDAGGWT 251
RESULT 14
AAR27756
ID AAR27756 standard; protein; 261 AA.
XX AC AAR27756;
XX DT 11-MAR-1993 (first entry)
XX DE NAD affinity glucose dehydrogenase.
XX KW GDH; glucose; recombinant.
XX OS Bacillus megaterium.
XX XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 96
XX FT /label= Glu, Leu
XX FT Misc-difference 258
XX FT /label= Thr, Ala
XX PN JP04258289-A.
XX PD 14-SEP-1992.
XX PF 13-FEB-1991; 91JP-0187085.
XX XX
XX PR 13-FEB-1991; 91JP-0187085.
```

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XX PA (AMAN ) AMANO PHARM KK.
XX DR WPI; 1992-354681/43.
XX DR N-PSDB; AAQ29486.
XX XX
XX PT New NAD affinity glucose dehydrogenase - obtd. from Bacillus
XX PT megaterium
XX PS Disclosure; Page 5; 8pp; Japanese.
XX CC The Bacillus megaterium derived NAD affinity glucose dehydrogenase
XX CC may be prepd. recombinantly by inserting its gene into a vector and
XX CC using this to transform E. coli. The enzyme may be used in a kit to
XX CC determine the amt. of glucose in a sample.
XX SQ Sequence 261 AA;
Query Match 27.9%; Score 359.5; DB 13; Length 261;
Best Local Similarity 31.9%; Pred. No. 1e-26;
Matches 83; Conservative 48; Mismatches 110; Indels 19; Gaps 4;
QY 1 MSNRLDGKVAITGGTGLGIGLAIAATKFEVEGAKVMT-----DRHSDVGEKAASV 51
DB 1 MYTDLKDKVVVITGGSTGLGRAMAVRFGOEAKVVIYNNNEEALDAKVEVEAGGQAI 60
QY 52 GTPDQIQFFQHDSSDEDGWTKLFDATKAFGPVSTLVNAGIAVNSKVSVEETTTAEWRKLL 111
DB 61 -----IVQGDVTKEDVVNLVQTAKEFTLDVMINNAGVENPVPSELSLDNKNKVI 113
QY 112 AVNLGDSVFFTRIGIORMKNGKLGASIIINSSIEGFGVDPGLGAYNASKGAVRIMSKSA 171
DB 114 DTNLGTGAFGLSRAIKFYFVENDIKGVINSSVHEMIPWFLFVHYAASKGKMXMTETLA 173
QY 172 LDCALKDYDVRVTVHPGYIKTPL-VDDLPGAEEAMSQRTKTPMGHIGEPNDIAYICVYL 230
DB 174 LEYAPK--GIRVNNIGPGAINTPINAKEFPADPVERADVESMIPMGYIGRPEEVAANAFL 231
QY 231 ASNESKFATGSEFVVDGGYT 250
DB 232 ASSEASVTVGTLFDAGGWT 251
RESULT 15
AAP80590
ID AAP80590 standard; protein; 261 AA.
XX AC AAP80590;
XX DT 14-SEP-1990 (first entry)
XX DE Sequence of glucose dehydrogenase (GD) from Bacillus megaterium as
XX DE encoded on plasmid pJH11.
XX KW Bacillus megaterium; non-pathogenic; glucose dehydrogenase;
XX KW plasmid pSA677 (DSM 4055P); plasmid pSAG2 (DSM 4054P);
XX KW plasmid pSAC4 (DSM 4053P); B. megaterium strain M1296/pSAC7 (DSM 4050);
XX KW B. megaterium strain M1296/pSAC2 (DSM 4048); high protein yields;
XX KW B. megaterium strain M1296/pSAC4 (DSM 4049); plasmid pJH11.
XX OS Bacillus megaterium.
XX PN EP285949-A.
XX PD 12-OCT-1988.
XX PF 28-MAR-1988; 88EP-0104953.
XX PR 08-APR-1987; 87DE-3711883.
XX XX
XX PA (MERE ) MERCK PATENT GMBH.
XX PI Ebeling W, Heilmann HJ, Meinhardt F;
```


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OM protein - protein search, using sw model

Run on: October 30, 2002, 15:45:40 ; Search time 32 Seconds

(without alignments)
874.706 Million cell updates/sec

Title: US-09-910-033a-2

Perfect score: 252

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 0

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	179	71.0	252	18 AAW23407	Lactobacillus brev
2	47	18.7	251	18 AAW23409	Lactobacillus kefi
3	36	14.3	50	20 AAY30523	L. brevis ADH N-te
4	36	14.3	50	20 AAY33419	L. brevis wild-typ
5	28	11.1	50	20 AAY33424	L. brevis ADH pept
6	27	10.7	50	20 AAY33420	L. brevis ADH pept
7	27	10.7	50	20 AAY33421	L. brevis ADH pept
8	27	10.7	50	20 AAY33422	L. brevis ADH pept
9	27	10.7	50	20 AAY33423	L. brevis ADH pept
10	25	9.9	38	18 AAW23408	Lactobacillus kefi
11	20	7.9	34	20 AAY33413	L. brevis NADP-dep

12	8	3.2	120	22	ABG07478	Novel human diagno
13	8	3.2	120	22	ABB40547	Peptide #8053 enco
14	8	3.2	120	22	AAW74176	Human bone marrow
15	8	3.2	136	22	AAU55352	Propionibacterium
16	8	3.2	241	22	AAW70963	S. spinosa protein
17	8	3.2	254	22	AAW49773	Protein with acety
18	8	3.2	254	22	AAW47522	(R)-2-octanol dehy
19	8	3.2	255	20	AAW39316	ORF115 protein inv
20	8	3.2	258	22	AAW2682	C glutamicum prote
21	8	3.2	258	22	AAW79361	Corynebacterium gl
22	8	3.2	272	21	AAW09589	Arabidopsis thalia
23	8	3.2	272	21	AAW77928	A. thaliana enviro
24	8	3.2	275	21	AAW09588	Arabidopsis thalia
25	8	3.2	277	19	AAW51011	Human liver carbon
26	8	3.2	317	21	AAW50903	Tomato nicotinamin
27	8	3.2	336	16	AAW06488	Maize f52 sequence
28	8	3.2	377	21	AAW06248	Arabidopsis thalia
29	8	3.2	397	21	AAW06247	Arabidopsis thalia
30	8	3.2	485	15	AAW47812	Sequence of amino
31	8	3.2	485	21	AAW06246	Arabidopsis thalia
32	8	3.2	559	22	AAW07374	Novel human diagno
33	7	2.8	15	22	AAW67050	Human proton trans
34	7	2.8	33	21	AAW67477	S. clava antimicro
35	7	2.8	33	21	AAW67479	S. clava antimicro
36	7	2.8	34	22	AAW51232	E. coli AMP gene S
37	7	2.8	123	22	AAW40180	Peptide #7686 enco
38	7	2.8	123	22	AAW60948	Human brain expres
39	7	2.8	123	22	AAW73641	Human bone marrow
40	7	2.8	123	22	AAW33832	Peptide #7869 enco
41	7	2.8	127	18	AAW11213	S. pneumoniae 3-ox
42	7	2.8	132	21	AAW52575	Amino acid sequenc
43	7	2.8	133	22	AAW82489	S. epidermidis ope
44	7	2.8	140	21	AAW41413	Human ORFX ORF1177
45	7	2.8	171	22	AAW82281	S. epidermidis ope

ALIGNMENTS

RESULT 1
AAW23407
ID AAW23407 standard; Protein; 252 AA.

XX AAW23407;
XX
XX
XX
DT 27-MAR-1998 (first entry)
XX
XX Lactobacillus brevis alcohol dehydrogenase.
DE Alcohol dehydrogenase; production; (R)-alcohol; (S)-alcohol.
KW
XX
XX Lactobacillus brevis.
OS

XX
PN EP796914-A2.
XX
PD 24-SEP-1997.
XX
PF 20-MAR-1997; 97EP-0104814.
XX
PR 21-MAR-1996; 96DE-4010984.
XX
PA (BOEF) BOEHRINGER MANNHEIM GMBH.

XX
PI Hummel W, Riebel B;
XX
DR WPI; 1997-459831/43.
DR N-PSDB; AAT73132.
XX
PT Lactobacillus brevis alcohol dehydrogenase - useful for production
PT of optically active alcohol(s)
XX
PS Claim 8; Pages 24-26; 34pp; German.
XX

Best Local Similarity 100.0%; Pred. No. 1.6e-38;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 153 LGAYNASKGAVRIMSKSAALDCALKDYDVRVNTVHPGYIKTPLVDDL 199
|||||
DB 152 LGAYNASKGAVRIMSKSAALDCALKDYDVRVNTVHPGYIKTPLVDDL 198

RESULT 3
AAV30523
ID AAY30523 standard; peptide; 50 AA.
XX AC AAY30523;
XX DT 03-DEC-1999 (first entry)
XX DE L. brevis ADH N-terminal peptide fragment.
XX KW ADH; alcohol dehydrogenase; NADH-specificity; coenzyme docking region;
KW NADPH-dependent dehydrogenase; stereo-selective extraction; racemic;
KW R-hydroxy-compound; keto-compound; S-hydroxy-compound.
XX OS Lactobacillus brevis.
XX PN WO9947684-A2.
XX DT 23-SEP-1999.
XX PF 18-MAR-1999; 99WO-DE00848.
XX PR 19-MAR-1998; 98DE-1012004.
XX PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX PI Hummel W, Riebel B;
XX DR WPI; 1999-571842/48.
XX PT Improving NADH-specificity of NADPH-dependent dehydrogenases by
XX PT recombinant microbial techniques -
XX PS Disclosure; Page 2; 35pp; German.

Query Match 14.3%; Score 36; DB 20; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.5e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SNRLDGKVAITGGTIGLIGLAIATKFEVGEAKVMIT 37
|||||
DB 1 SNRLDGKVAITGGTIGLIGLAIATKFEVGEAKVMIT 36

RESULT 4
AAV33419
ID AAY33419 standard; peptide; 50 AA.
XX AC AAV33419;
XX DT 03-DEC-1999 (first entry)

XX DE L. brevis wild-type ADH peptide fragment.
XX KW ADH; alcohol dehydrogenase; NADH-specificity; coenzyme docking region;
KW NADPH-dependent dehydrogenase; stereo-selective extraction; racemic;
KW R-hydroxy-compound; keto-compound; S-hydroxy-compound; mutant.
XX OS Lactobacillus brevis.
XX PN WO9947684-A2.
XX DT 23-SEP-1999.
XX PF 18-MAR-1999; 99WO-DE00848.
XX PR 19-MAR-1998; 98DE-1012004.
XX PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX PI Hummel W, Riebel B;
XX DR WPI; 1999-571842/48.
XX PT Improving NADH-specificity of NADPH-dependent dehydrogenases by
XX PT recombinant microbial techniques -
XX PS Claim 10; Page 30; 35pp; German.
XX CC This invention describes a novel method for improving NADH-specificity of
CC preferred NADPH-dependent dehydrogenase. The method comprises a reduction
CC in the basicity of the coenzyme-docking region of the enzyme through
CC alteration of the relevant amino acid sequence using genetic technology.
CC The improved dehydrogenase can be used for stereo-selective extraction of
CC R-hydroxy-compounds through enzymatic reduction of the corresponding
CC keto-compound. They can also be used for stereo-selective extraction of
CC S-hydroxy-compounds from racemic mixtures, through enzymatic oxidation of
CC the R-hydroxy-compound. The dehydrogenases have improved temperature and
CC pH optimums and improved stability. This sequence represents a wild-type
CC Lactobacillus brevis alcohol dehydrogenase (ADH) peptide fragment.

Query Match 14.3%; Score 36; DB 20; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.5e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SNRLDGKVAITGGTIGLIGLAIATKFEVGEAKVMIT 37
|||||
DB 1 SNRLDGKVAITGGTIGLIGLAIATKFEVGEAKVMIT 36

RESULT 5
AAV33424
ID AAY33424 standard; peptide; 50 AA.
XX AC AAY33424;
XX DT 03-DEC-1999 (first entry)
XX DE L. brevis ADH peptide fragment mutant 2/3.
XX KW ADH; alcohol dehydrogenase; NADH-specificity; coenzyme docking region;
KW NADPH-dependent dehydrogenase; stereo-selective extraction; racemic;
KW R-hydroxy-compound; keto-compound; S-hydroxy-compound; mutant.
XX OS Lactobacillus brevis.
XX OS Synthetic.
XX PN WO9947684-A2.
XX DT 23-SEP-1999.
XX PF 18-MAR-1999; 99WO-DE00848.

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XX PR 19-MAR-1998; 98DE-1012004.
XX PA (KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX PI Hummel W, Riebel B;
XX XX WPI; 1999-571842/48.
XX PT Improving NADH-specificity of NADPH-dependent dehydrogenases by
XX PT recombinant microbial techniques -
XX PS Claim 10; Page 30; 35pp; German.
XX SQ Sequence 50 AA;
CC This invention describes a novel method for improving NADH-specificity of
CC preferred NADPH-dependent dehydrogenase. The method comprises a reduction
CC in the basicity of the coenzyme-docking region of the enzyme through
CC alteration of the relevant amino acid sequence using genetic technology.
CC The improved dehydrogenase can be used for stereo-selective extraction of
CC R-hydroxy-compounds through enzymatic reduction of the corresponding
CC keto-compound. They can also be used for stereo-selective extraction of
CC S-hydroxy-compounds from racemic mixtures, through enzymatic oxidation of
CC the R-hydroxy-compound. The dehydrogenases have improved temperature and
CC pH optimums and improved stability. This sequence represents a mutant
CC Lactobacillus brevis alcohol dehydrogenase (ADH) peptide fragment.
XX SQ Sequence 50 AA;
CC Query Match 11.1%; Score 28; DB 20; Length 50;
CC Best Local Similarity 100.0%; Pred. No. 3.3e-20;
CC Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 IITGGTIGIGLAIAATKFEVSGAKVMITD 38
DB 10 IITGGTIGIGLAIAATKFEVSGAKVMITD 37
RESULT 6
AY33420
ID AAY33420 standard; peptide; 50 AA.
XX AC AAY33420;
XX XX 03-DEC-1999 (first entry)
XX DT L. brevis ADH peptide fragment mutant 1.
XX DE ADH; alcohol dehydrogenase; NADH-specificity; coenzyme docking region;
XX KW NADPH-dependent dehydrogenase; stereo-selective extraction; racemic;
XX KW R-hydroxy-compound; keto-compound; S-hydroxy-compound; mutant.
XX OS Lactobacillus brevis.
XX OS Synthetic.
XX PN WO9947684-A2.
XX XX 23-SEP-1999.
XX PD 18-MAR-1999; 99WO-DE00848.
XX PF 19-MAR-1998; 98DE-1012004.
XX PR (KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX PA Hummel W, Riebel B;
XX PI WPI; 1999-571842/48.
XX XX Improving NADH-specificity of NADPH-dependent dehydrogenases by
XX XX recombinant microbial techniques -
XX PS Claim 10; Page 30; 35pp; German.
XX SQ Sequence 50 AA;
CC This invention describes a novel method for improving NADH-specificity of
CC preferred NADPH-dependent dehydrogenase. The method comprises a reduction
CC in the basicity of the coenzyme-docking region of the enzyme through
CC alteration of the relevant amino acid sequence using genetic technology.
CC The improved dehydrogenase can be used for stereo-selective extraction of
CC R-hydroxy-compounds through enzymatic reduction of the corresponding
CC keto-compound. They can also be used for stereo-selective extraction of
CC S-hydroxy-compounds from racemic mixtures, through enzymatic oxidation of
CC the R-hydroxy-compound. The dehydrogenases have improved temperature and
CC pH optimums and improved stability. This sequence represents a mutant
CC Lactobacillus brevis alcohol dehydrogenase (ADH) peptide fragment.
XX SQ Sequence 50 AA;
CC Query Match 11.1%; Score 28; DB 20; Length 50;
CC Best Local Similarity 100.0%; Pred. No. 3.3e-20;
CC Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 IITGGTIGIGLAIAATKFEVSGAKVMITD 38
DB 10 IITGGTIGIGLAIAATKFEVSGAKVMITD 37
RESULT 7
AY33421
ID AAY33421 standard; peptide; 50 AA.
XX AC AAY33421;
XX XX 03-DEC-1999 (first entry)
XX DT L. brevis ADH peptide fragment mutant 1/1.
XX DE ADH; alcohol dehydrogenase; NADH-specificity; coenzyme docking region;
XX KW NADPH-dependent dehydrogenase; stereo-selective extraction; racemic;
XX KW R-hydroxy-compound; keto-compound; S-hydroxy-compound; mutant.
XX OS Lactobacillus brevis.
XX OS Synthetic.
XX PN WO9947684-A2.
XX XX 23-SEP-1999.
XX PD 18-MAR-1999; 99WO-DE00848.
XX PF 19-MAR-1998; 98DE-1012004.
XX PR (KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX PA Hummel W, Riebel B;
XX PI WPI; 1999-571842/48.
XX XX Improving NADH-specificity of NADPH-dependent dehydrogenases by
XX XX recombinant microbial techniques -
XX PS Claim 10; Page 30; 35pp; German.
XX SQ Sequence 50 AA;
CC This invention describes a novel method for improving NADH-specificity of
CC preferred NADPH-dependent dehydrogenase. The method comprises a reduction
CC in the basicity of the coenzyme-docking region of the enzyme through
CC alteration of the relevant amino acid sequence using genetic technology.
CC The improved dehydrogenase can be used for stereo-selective extraction of
CC R-hydroxy-compounds through enzymatic reduction of the corresponding
CC keto-compound. They can also be used for stereo-selective extraction of
CC S-hydroxy-compounds from racemic mixtures, through enzymatic oxidation of
CC the R-hydroxy-compound. The dehydrogenases have improved temperature and
CC pH optimums and improved stability. This sequence represents a mutant
CC Lactobacillus brevis alcohol dehydrogenase (ADH) peptide fragment.
XX SQ Sequence 50 AA;

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CC This invention describes a novel method for improving NADH-specificity of
CC preferred NADPH-dependent dehydrogenase. The method comprises a reduction
CC in the basicity of the coenzyme-docking region of the enzyme through
CC alteration of the relevant amino acid sequence using genetic technology.
CC The improved dehydrogenase can be used for stereo-selective extraction of
CC R-hydroxy-compounds through enzymatic reduction of the corresponding
CC keto-compound. They can also be used for stereo-selective extraction of
CC S-hydroxy-compounds from racemic mixtures, through enzymatic oxidation of
CC the R-hydroxy-compound. The dehydrogenases have improved temperature and
CC pH optimums and improved stability. This sequence represents a mutant
CC Lactobacillus brevis alcohol dehydrogenase (ADH) peptide fragment.
XX SQ Sequence 50 AA;

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Query Match 10.7%; Score 27; DB 20; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.3e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 IITGGTIGIGLAIAATKFEVSGAKVMIT 37
DB 10 IITGGTIGIGLAIAATKFEVSGAKVMIT 36

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RESULT 7
AY33421
ID AAY33421 standard; peptide; 50 AA.
XX AC AAY33421;
XX XX 03-DEC-1999 (first entry)
XX DT L. brevis ADH peptide fragment mutant 1/1.
XX DE ADH; alcohol dehydrogenase; NADH-specificity; coenzyme docking region;
XX KW NADPH-dependent dehydrogenase; stereo-selective extraction; racemic;
XX KW R-hydroxy-compound; keto-compound; S-hydroxy-compound; mutant.
XX OS Lactobacillus brevis.
XX OS Synthetic.
XX PN WO9947684-A2.
XX XX 23-SEP-1999.
XX PD 18-MAR-1999; 99WO-DE00848.
XX PF 19-MAR-1998; 98DE-1012004.
XX PR (KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX PA Hummel W, Riebel B;
XX PI WPI; 1999-571842/48.
XX XX Improving NADH-specificity of NADPH-dependent dehydrogenases by
XX XX recombinant microbial techniques -
XX PS Claim 10; Page 30; 35pp; German.
XX SQ Sequence 50 AA;

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```

CC This invention describes a novel method for improving NADH-specificity of
CC preferred NADPH-dependent dehydrogenase. The method comprises a reduction
CC in the basicity of the coenzyme-docking region of the enzyme through
CC alteration of the relevant amino acid sequence using genetic technology.
CC The improved dehydrogenase can be used for stereo-selective extraction of
CC R-hydroxy-compounds through enzymatic reduction of the corresponding
CC keto-compound. They can also be used for stereo-selective extraction of
CC S-hydroxy-compounds from racemic mixtures, through enzymatic oxidation of
CC the R-hydroxy-compound. The dehydrogenases have improved temperature and
CC pH optimums and improved stability. This sequence represents a mutant
CC Lactobacillus brevis alcohol dehydrogenase (ADH) peptide fragment.
XX SQ Sequence 50 AA;

```

Query Match 10.7%; Score 27; DB 20; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.3e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 IITGTLGIGLAIAIKFVEEGAKVMIT 37
DB 10 IITGTLGIGLAIAIKFVEEGAKVMIT 36

RESULT 8
AAV33422
ID AAV33422 standard; peptide; 50 AA.
XX
AC AAV33422;
XX
DT 03-DEC-1999 (first entry)
XX
DE L. brevis ADH peptide fragment mutant 2.
XX
KW ADH; alcohol dehydrogenase; NADH-specificity; coenzyme docking region;
KW NADPH-dependent dehydrogenase; stereo-selective extraction; racemic;
KW R-hydroxy-compound; keto-compound; S-hydroxy-compound; mutant.
XX
OS Lactobacillus brevis.
OS Synthetic.
XX
PN WO9947684-A2.
XX
PD 23-SEP-1999.
XX
PF 18-MAR-1999; 99WO-DE00848.
XX
PR 19-MAR-1998; 98DE-1012004.
XX
PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX
PI Hummel W, Riebel B;
XX
DR WPI; 1999-571842/48.
XX
PT Improving NADH-specificity of NADPH-dependent dehydrogenases by
PT recombinant microbial techniques -
XX
PS Claim 10; Page 30; 35pp; German.
XX
SQ This invention describes a novel method for improving NADH-specificity of
CC preferred NADPH-dependent dehydrogenase. The method comprises a reduction
CC in the basicity of the coenzyme-docking region of the enzyme through
CC alteration of the relevant amino acid sequence using genetic technology.
CC The improved dehydrogenase can be used for stereo-selective extraction of
CC R-hydroxy-compounds through enzymatic reduction of the corresponding
CC keto-compound. They can also be used for stereo-selective extraction of
CC S-hydroxy-compounds from racemic mixtures, through enzymatic oxidation of
CC the R-hydroxy-compound. The dehydrogenases have improved temperature and
CC pH optimums and improved stability. This sequence represents a mutant
CC Lactobacillus brevis alcohol dehydrogenase (ADH) peptide fragment.

Query Match 10.7%; Score 27; DB 20; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.3e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 IITGTLGIGLAIAIKFVEEGAKVMIT 37
DB 10 IITGTLGIGLAIAIKFVEEGAKVMIT 36

RESULT 9
AAV33423
ID AAV33423 standard; peptide; 50 AA.
XX
AC AAV33423;

XX 03-DEC-1999 (first entry)
XX L. brevis ADH peptide fragment mutant 2/2.
XX
KW ADH; alcohol dehydrogenase; NADH-specificity; coenzyme docking region;
KW NADPH-dependent dehydrogenase; stereo-selective extraction; racemic;
KW R-hydroxy-compound; keto-compound; S-hydroxy-compound; mutant.
XX
OS Lactobacillus brevis.
OS Synthetic.
XX
PN WO9947684-A2.
XX
PD 23-SEP-1999.
XX
PF 18-MAR-1999; 99WO-DE00848.
XX
PR 19-MAR-1998; 98DE-1012004.
XX
PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX
PI Hummel W, Riebel B;
XX
DR WPI; 1999-571842/48.
XX
PT Improving NADH-specificity of NADPH-dependent dehydrogenases by
PT recombinant microbial techniques -
XX
PS Claim 10; Page 30; 35pp; German.
XX
SQ This invention describes a novel method for improving NADH-specificity of
CC preferred NADPH-dependent dehydrogenase. The method comprises a reduction
CC in the basicity of the coenzyme-docking region of the enzyme through
CC alteration of the relevant amino acid sequence using genetic technology.
CC The improved dehydrogenase can be used for stereo-selective extraction of
CC R-hydroxy-compounds through enzymatic reduction of the corresponding
CC keto-compound. They can also be used for stereo-selective extraction of
CC S-hydroxy-compounds from racemic mixtures, through enzymatic oxidation of
CC the R-hydroxy-compound. The dehydrogenases have improved temperature and
CC pH optimums and improved stability. This sequence represents a mutant
CC Lactobacillus brevis alcohol dehydrogenase (ADH) peptide fragment.

Query Match 10.7%; Score 27; DB 20; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.3e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 IITGTLGIGLAIAIKFVEEGAKVMIT 37
DB 10 IITGTLGIGLAIAIKFVEEGAKVMIT 36

RESULT 10
AAW23408
ID AAW23408 standard; peptide; 38 AA.
XX
AC AAW23408;
XX
DT 27-MAR-1998 (first entry)
XX
DE Lactobacillus kefir alcohol dehydrogenase amino-terminal.
XX
KW Alcohol dehydrogenase; production; (R)-alcohol; (S)-alcohol;
KW amino-terminal.
XX
OS Lactobacillus kefir.
XX
PN EP796914-A2.
XX
PD 24-SEP-1997.
XX

PP 20-MAR-1997; 97EP-0104814.
 XX 21-MAR-1996; 96DE-4010984.
 PR (BOEF) BOEHRINGER MANNHEIM GMBH.
 PA Hummel W, Riebel B;
 XX WPI; 1997-459831/43.
 PI Lactobacillus brevis alcohol dehydrogenase - useful for production
 XX of optically active alcohol(s)
 PT Example 3; Page 12; 34pp; German.
 PS The present Lactobacillus kefir alcohol dehydrogenase (ADH)
 XX amino-terminal sequence was used in the isolation of a L. brevis
 CC ADH, which retains at least 95% of its activity after 30
 CC minutes at 20-60 degrees C and can be purified to a specific
 CC activity of at least 400 U/mg. The enzyme can be used to produce
 CC (R)-alcohols by enantioselective reduction of ketones of formula
 CC R1-CO-R2, where R1 and R2 = hydrogen (sic) or 1-20C alkyl, alkenyl,
 CC aryl or arylethyl (sic) optionally substituted by halogen, NO2, OH
 CC or 1-20C alkoxy, an optionally substituted 1-10C alkylene group,
 CC which is substituted by saturated, unsaturated or aromatic
 CC nitrogen, oxygen or sulphur heterocycles, or may be an optionally
 CC substituted polycondensed saturated and/or aromatic group* (sic) in
 CC the presence of the enzyme or cells containing it at 20-60 degrees
 CC C for 0.25-3 hours, or (S)-alcohols by incubating it at 20-60 degrees
 CC of formula R1-CHOH-R2 in the presence of the enzyme or cells
 CC containing it at 20-60 degrees C for 0.25-3 hours.
 XX Sequence 38 AA;
 SQ

Query Match 9.9%; Score 25; DB 18; Length 38;
 Best Local Similarity 100.0%; Pred. No. 2.5e-17;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 TGGTGLGIGLAIAATKFFVEEGAKVMIT 37
 Db 12 TGGTGLGIGLAIAATKFFVEEGAKVMIT 36
 RESULT 11
 AAY33413
 ID AAY33413 standard; Protein; 34 AA.
 XX
 AC AAY33413;
 XX
 DT 03-DEC-1999 (first entry)
 XX
 DE L. brevis NADP-dependent oxidoreductase peptide fragment 1.
 XX
 KW ADH; alcohol dehydrogenase; NADH-specificity; coenzyme docking region;
 KW NADPH-dependent dehydrogenase; stereo-selective docking region;
 KW R-hydroxy-compound; keto-compound; S-hydroxy-compound.
 XX
 OS Lactobacillus brevis.
 XX
 PN WO9947684-A2.
 XX
 PD 23-SEP-1999.
 XX
 PF 18-MAR-1999; 99WO-DE00848.
 XX
 PR 19-MAR-1998; 98DE-1012004.
 XX
 PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
 XX
 PI Hummel W, Riebel B;
 XX
 DR WPI; 1999-571842/48.
 XX

Improving NADH-specificity of NADPH-dependent dehydrogenases by
 recombinant microbial techniques -
 Example 4; Page 27; 35pp; German.
 This invention describes a novel method for improving NADH-specificity of
 preferred NADPH-dependent dehydrogenase. The method comprises a reduction
 in the basicity of the coenzyme-docking region of the enzyme through
 alteration of the relevant amino acid sequence using genetic technology.
 The improved dehydrogenase can be used for stereo-selective extraction of
 R-hydroxy-compounds through enzymatic reduction of the corresponding
 keto-compound. They can also be used for stereo-selective extraction of
 S-hydroxy-compounds from racemic mixtures, through enzymatic oxidation of
 the R-hydroxy-compound. The dehydrogenases have improved temperature and
 pH optimums and improved stability. This sequence represents a
 Lactobacillus brevis alcohol dehydrogenase (ADH) coenzyme binding site
 described in the method of the invention.
 XX Sequence 34 AA;
 SQ

Query Match 7.9%; Score 20; DB 20; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.2e-12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 GIGLAIAATKFFVEEGAKVMIT 37
 Db 1 GIGLAIAATKFFVEEGAKVMIT 20
 RESULT 12
 ABG07478
 ID ABG07478 standard; Protein; 120 AA.
 XX
 AC ABG07478;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #7459.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS71665.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID No 37837; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques

CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 120 AA;
Query Match 3.2%; Score 8; DB 22; Length 120;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 86 TLVNNAGI 93
Db 82 TLVNNAGI 89
|||||

RESULT 13
ABB40547
ID ABB40547 standard; Peptide; 120 AA.

AC ABB40547;

XX DT 04-FEB-2002 (first entry)

DE Peptide #8053 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

XX OS Homo sapiens.

XX PN WO200157277-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US00669.

XX PR 04-FEB-2000; 2000US-0180312.

XX PR 26-MAY-2000; 2000US-0207456.

XX PR 30-JUN-2000; 2000US-0608408.

XX PR 03-AUG-2000; 2000US-0632366.

XX PR 21-SEP-2000; 2000US-0234687.

XX PR 27-SEP-2000; 2000US-0236359.

XX PR 04-OCT-2000; 2000GB-0024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-483447/52.

XX PT Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human foetal liver -

XX PS Claim 27; SEQ ID NO 33182; 639pp + sequence listing; English.

XX CC The invention relates to a single exon nucleic acid probe for
XX measuring human gene expression in a sample derived from human foetal
XX liver. The single exon nucleic acid probes may be used for predicting,
XX measuring and displaying gene expression in samples derived from human
XX foetal liver. The present sequence is a peptide encoded by a single exon
XX nucleic acid probe of the invention.
XX Note: The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 120 AA;

Query Match 3.2%; Score 8; DB 22; Length 120;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 87 LVNNAGIA 94
Db 87 LVNNAGIA 94
|||||

RESULT 14
AAM74176

ID AAM74176 standard; Protein; 120 AA.

XX AC AAM74176;

XX DT 06-NOV-2001 (first entry)

XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34482.

XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma.

XX OS Homo sapiens.

XX PN WO200157276-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US00668.

XX PR 04-FEB-2000; 2000US-0180312.

XX PR 26-MAY-2000; 2000US-0207456.

XX PR 30-JUN-2000; 2000US-0608408.

XX PR 03-AUG-2000; 2000US-0632366.

XX PR 21-SEP-2000; 2000US-0234687.

XX PR 27-SEP-2000; 2000US-0236359.

XX PR 04-OCT-2000; 2000GB-0024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-488900/53.

XX PT Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human bone marrow -

XX PS Example 4; SEQ ID NO: 34482; 658pp + Sequence Listing; English.

XX CC The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukaemia and myeloma. The present sequence is a
XX protein encoded by one of the probes of the invention.

XX SQ Sequence 120 AA;

Query Match 3.2%; Score 8; DB 22; Length 120;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 87 LVNNAGIA 94
Db 87 LVNNAGIA 94
|||||

RESULT 15

Job time : 34 secs

AAU5352
ID AAU5352 standard; Protein; 136 AA.
XX AC AAU5352;
XX DT 27-FEB-2002 (first entry)
XX DE
XX DE Propionibacterium acnes immunogenic protein #16248.
XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
XX KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
XX KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
XX KW dermatological; osteopathic; neuroprotectant.
XX OS
XX OS Propionibacterium acnes.
XX PN WO200181581-A2.
XX PD 01-NOV-2001.
XX PF 20-APR-2001; 2001WO-US12865.
XX PF 21-APR-2000; 2000US-199047P.
XX PR 02-JUN-2000; 2000US-208841P.
XX PR 07-JUL-2000; 2000US-216747P.
XX PA (CORI-) CORIXA CORP.
XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
XX PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX DR WPI; 2001-616774/71.
XX DR N-PSDB; AAS59569.
XX PT Propionibacterium acnes polypeptides and nucleic acids useful for
XX PT vaccinating against and diagnosing infections, especially useful for
XX PT treating acne vulgaris -
XX PS Example 1; SEQ ID No 16547; 1069pp; English.
XX CC Sequences AAU39105-AAU69017 represent Propionibacterium acnes immunogenic
XX CC polypeptides. The proteins and their associated DNA sequences are used in
XX CC the treatment, prevention and diagnosis of medical conditions caused by
XX CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
XX CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
XX CC P. acnes is also involved in infections of bone, joints and the central
XX CC nervous system, however it is particularly involved in the inflammatory
XX CC lesions associated with acne vulgaris. A method for detecting the
XX CC presence or absence of P. acnes in a patient comprises contacting a
XX CC sample with a binding agent that binds to the proteins of the invention
XX CC and determining the amount of bound protein in the sample. The
XX CC polypeptides may be used as antigens in the production of antibodies
XX CC specific for P. acnes proteins. These antibodies can be used to
XX CC downregulate expression and activity of P. acnes polypeptides and
XX CC therefore treat P. acnes infections. The antibodies may also be used as
XX CC diagnostic agents for determining P. acnes presence, for example, by
XX CC enzyme linked immunosorbent assay (ELISA).
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 136 AA;
Query Match 3.2%; Score 8; DB 22; Length 136;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 88 VNNAGIAY 95
DB 34 VNNAGIAY 41
|||||||
Search completed: October 30, 2002, 15:48:00

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OM protein - protein search, using sw model

Run on: October 30, 2002, 15:46:30 ; Search time 19 Seconds
(without alignments)
1274.448 Million cell updates/sec

Title: US-09-910-033A-2
Perfect score: 252
Sequence: 1 MSNRDQKVAITGTLGIG.....NESKFGSEFVDDGGYTAQ 252

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	4.0	29	2 S14099	12-alpha-hydroxyst
2	10	4.0	260	2 B87668	2-deoxy-D-gluconat
3	9	3.6	250	2 T02058	hypothetical prote
4	9	3.6	267	2 T11579	probable short cha
5	9	3.6	283	2 E87603	hypothetical prote
6	9	3.6	289	2 D69825	glucose 1-dehydrog
7	9	3.6	303	2 T46064	short-chain alcoh
8	8	3.2	238	2 G83126	probable short-cha
9	8	3.2	249	2 S47055	hypothetical prote
10	8	3.2	251	2 T4180	hypothetical prote
11	8	3.2	251	2 T06364	probable short-cha
12	8	3.2	251	2 AC0103	2-deoxy-D-gluconat
13	8	3.2	252	2 D83766	3-oxoacyl-(acyl-ca
14	8	3.2	252	2 G72618	hypothetical prote
15	8	3.2	254	2 B87630	hypothetical prote
16	8	3.2	254	2 A03182	short chain dehydr
17	8	3.2	257	2 C98348	reductase (AL13282
18	8	3.2	257	2 AD2934	short chain dehydr
19	8	3.2	263	2 A98301	probable short-cha
20	8	3.2	263	2 AG2982	dehydrogenase Atu3
21	8	3.2	272	2 T47354	alcohol dehydrogen
22	8	3.2	276	2 JC5285	carboxyl reductase
23	8	3.2	277	1 RDHUCB	carboxyl reductase
24	8	3.2	277	2 JC5284	carboxyl reductase
25	8	3.2	277	2 T29800	hypothetical prote
26	8	3.2	307	2 S62472	probable Methylthi
27	8	3.2	335	2 T24540	hypothetical prote
28	8	3.2	336	2 A47542	short-chain alcoh
29	8	3.2	475	2 T00620	probable amino aci

amino acid transpo
oxidoreductase hom
ntpQ protein - Ent
hemoglobin alpha-2
hemoglobin alpha-I
hemoglobin alpha-I
hemoglobin alpha c
hemoglobin alpha c
3-octaprenyl-4-hyd
ribosomal protein
ribosomal protein
hypothetical prote
3-hydroxybutyrate
shikimate kinase I
hypothetical prote
pyrrolidone carbox

ALIGNMENTS

RESULT 1

S14099
12-alpha-hydroxysteroid dehydrogenase - Clostridium sp. (strain C 48-50)
C:Species: Clostridium sp.
A:Variety: strain C 48-50
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S14099
R: Braun, M.; Luensdorf, H.; Bueckmann, A.F.
Eur. J. Biochem. 196, 439-450, 1991
A:Title: 12-alpha-hydroxysteroid dehydrogenase from Clostridium group P, strain C 48-50
A:Reference number: S14099; MUID:91177018
A:Accession: S14099
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-29 <BRA>

Query Match 4.0%; Score 10; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DGKVAITGG 15
|||||

DB 4 DGKVAITGG 13
|||||

RESULT 2

B87668
2-deoxy-D-gluconate 3-dehydrogenase [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: B87668
R: Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kc n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: B87668
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-260 <STO>
A:Cross-references: GB:AE005673; NID:gl3425088; PIDN:AAK25342.1; GSPDB:GN00148
C:Genetics: CC3380

Query Match 4.0%; Score 10; DB 2; Length 260;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 LAVNLDGVFF 120
|||||

Db 116 LAVNLGVFF 125

RESULT 3

T20258 hypothetical protein C55A6.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000

C:Accession: T20258

R:Kershaw, J.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z19243

A:Accession: T20258

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-250 <N1>

A:Cross-references: EMBL:Z81051; PIDN:CAB02866.1; GSPDB:GN00023; CBSP:C55A6.6

A:Experimental source: clone C55A6

C:Genetics:

A:Gene: CBSP:C55A6.6

A:Map position: 5

A:Introns: 43/3; 99/3; 217/3

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.6%; Score 9; DB 2; Length 250;

Best Local Similarity 100.0%; Pred. No. 0.39;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 LVNAGIATV 95

Db 85 LVNAGIATV 93

|||||

RESULT 4

T11579

probable short chain alcohol dehydrogenase CPRD12, drought-inducible - cowpea

C:Species: Vigna unguiculata (cowpea)

C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 20-Jun-2000

C:Accession: T11579

R:Tuchi, S.; Yamaguchi-Shinozaki, K.; Urao, T.; Shinozaki, K.

J. Plant Res. 109, 415-424, 1996

A:Title: Characterization of two cDNAs for novel drought-inducible genes in the highly

A:Reference number: Z17293

A:Accession: T11579

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-267 <IUC>

A:Cross-references: EMBL:D88121

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.6%; Score 9; DB 2; Length 267;

Best Local Similarity 100.0%; Pred. No. 0.41;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GKVAITGG 15

Db 16 GKVAITGG 24

|||||

RESULT 5

E87603

hypothetical protein CC2861 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 03-Aug-2001

C:Accession: E87603

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

n, J.; Esmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.W.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete genome sequence of Caulobacter crescentus.

A:Reference number: AB87249; MUID:21173698; PMID:11259647

A:Accession: E87603

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-283 <STO>

A:Cross-references: GB:AE005673; NID:gl3424475; PIDN:AAK24825.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC2861

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.6%; Score 9; DB 2; Length 283;

Best Local Similarity 100.0%; Pred. No. 0.44;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 LVNAGIATV 95

Db 84 LVNAGIATV 92

|||||

RESULT 6

D69825

glucose 1-dehydrogenase homolog yhfF - Bacillus subtilis

C:Species: Bacillus subtilis

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

C:Accession: D69825

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; B

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;

A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; G

lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo,

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardit

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; M

Y.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scal

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchi

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yamamoto, K.; Yata, K.; Yoshic

A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtil

A:Reference number: A69580; MUID:98044033

A:Accession: D69825

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-289 <KUN>

A:Cross-references: GB:Z99109; GB:AL009126; NID:g2633260; PIDN:CAB12784.1; PID:g2633

A:Experimental source: Strain 168

C:Genetics:

A:Gene: yhfF

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

F; 46-225/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 3.6%; Score 9; DB 2; Length 289;

Best Local Similarity 100.0%; Pred. No. 0.45;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GKVAITGG 15

Db 45 GKVAITGG 53

|||||

RESULT 7

T46064

short-chain alcohol dehydrogenase-like protein - Arabidopsis thaliana

N:Alternate names: protein T18N14.60

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Mar-2000

C:Accession: T46064

R:Delseny, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, M.; Mewes, H.W.; Lemcke,

submitted to the Protein Sequence Database, December 1999

A:Reference number: Z23013

A:Accession: T46064

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-303

A:Cross-references: EMBL:AL132968

A:Experimental source: cultivar Columbia; BAC clone T18N14

C:Genetics:

A:Map position: 3

A:Introns: 31/2

A:Note: T18N14.60

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.6%; Score 9; DB 2; Length 303;

Best Local Similarity 100.0%; Pred. No. 0.46;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GKVAITGG 15

Db 34 GKVAITGG 42

RESULT 8

G83126

probable short-chain dehydrogenase PA4162 [imported] - Pseudomonas aeruginosa (strain PA

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: G83126

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoquchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: AB2950; MUID:20437337

A:Accession: G83126

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-238 <STO>

A:Cross-references: GB:AE004832; GB:AE004091; NID:g9950360; PIDN:AAG07549.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA4162

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.2%; Score 8; DB 2; Length 238;

Best Local Similarity 100.0%; Pred. No. 4;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 LVNNAGIA 94

Db 73 LVNNAGIA 80

RESULT 9

S47055

hypothetical protein 5 - Xanthobacter sp.

C:Species: Xanthobacter sp.

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999

C:Accession: S47055

R:Swaving, J.; Weijers, C.A.G.M.; van Ooyen, A.J.J.; de Bont, J.A.M.

submitted to the EMBL Data Library, June 1994

A:Description: Plasmid of Xanthobacter Py2 mutants in epoxylane degradation; exp

A:Reference number: S47051

A:Accession: S47055

A:Molecule type: DNA

A:Residues: 1-249 <SWA>

A:Cross-references: EMBL:X79863; NID:g520947; PIDN:CAA56245.1; PID:g520952

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

F:5-181/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 3.2%; Score 8; DB 2; Length 249;

Best Local Similarity 100.0%; Pred. No. 4.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 LVNNAGIA 94

Db 82 LVNNAGIA 89

RESULT 10

T24180

hypothetical protein R11D1.11 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000

C:Accession: T24180

R:Steward, C.

submitted to the EMBL Data Library, June 1996

A:Reference number: Z19850

A:Accession: T24180

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-251 <WIL>

A:Cross-references: EMBL:Z75547; PIDN:CAA99897.1; GSPDB:GN00023; CESP:R11D1.11

A:Experimental source: clone R11D1

C:Genetics:

A:Gene: CESP:R11D1.11

A:Map position: 5

A:Introns: 56/3; 157/1; 196/3

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.2%; Score 8; DB 2; Length 251;

Best Local Similarity 100.0%; Pred. No. 4.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 LVNNAGIA 94

Db 87 LVNNAGIA 94

RESULT 11

T06364

probable short-chain alcohol-dehydrogenase (EC 1.1.1.1-) - tomato (fragment)

C:Species: Lycopersicon esculentum (tomato)

C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000

C:Accession: T06364

R:Jacobsen, S.E.; Olszewski, N.E.

Planta 198, 78-86, 1996

A:Title: Gibberellins regulate the abundance of RNAs with sequence similarity to prot

A:Reference number: Z15627; MUID:96158488

A:Accession: T06364

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-251 <JAC>

A:Cross-references: EMBL:U21801; NID:g717141; PIDN:AAB00109.1; PID:g717142

A:Experimental source: cultivar Money-maker

C:Genetics:

A:Gene: GAD3

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

C:Keywords: alcohol metabolism; oxidoreductase

Query Match 3.2%; Score 8; DB 2; Length 251;

Best Local Similarity 100.0%; Pred. No. 4.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GKVAITG 14

Db 2 GKVAITG 9

RESULT 12

AC0103

2-deoxy-D-gluconate 3-dehydrogenase (EC 1.1.1.125) [imported] - Yersinia pestis (stra

C:Species: Yersinia pestis

C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001

C:Accession: AC0103

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, N

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G

il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell

Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AC0103

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-251 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC89686.1; PID:g15978913; GSPDB:GN00175

C:Genetics:

A:Gene: kduD2

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C:Keywords: oxidoreductase

Query Match 3.2%; Score 8; DB 2; Length 251;

Best Local Similarity 100.0%; Pred. No. 4.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GKVAITG 14

|||||

Db 8 GKVAITG 15

RESULT 13

D83766

3-oxoacyl-(acyl-carrier protein) reductase BH0932 [imported] - Bacillus halodurans (strain
C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C:Accession: D83766

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: D83766

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-252 <STO>

A:Cross-references: GB:AP001510; GB:BA000004; MID:g10173440; PIDN:BA04651.1; GSPDB:GN00

C:Experimental source: strain C-125

C:Genetics:

A:Gene: BH0932

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.2%; Score 8; DB 2; Length 252;

Best Local Similarity 100.0%; Pred. No. 4.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 FVEEGAKV 34

|||||

Db 27 FVEEGAKV 34

RESULT 14

G72618

hypothetical protein APE1408 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C:Accession: G72618

R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-do, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr

A:Reference number: A72450; MUID:99310339

A:Accession: G72618

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-252 <KAW>

A:Cross-references: DDBJ:AP000061; NID:g5104821; PIDN:BAA80405.1; PID:g5105091

C:Experimental source: strain K1

C:Genetics:

A:Gene: APE1408

C:Superfamily: Aeropyrum pernix hypothetical protein APE1408

Query Match 3.2%; Score 8; DB 2; Length 252;

Best Local Similarity 100.0%; Pred. No. 4.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 IEGFVGDP 151

Db 225 IEGFVGDP 232
|||||

RESULT 15

B87630

hypothetical protein CC3076 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001

C:Accession: B87630

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.;
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser,
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: B87630

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-254 <STO>

A:Cross-references: GB:AE005673; NID:g13424728; PIDN:AAK25038.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC3076

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.2%; Score 8; DB 2; Length 254;

Best Local Similarity 100.0%; Pred. No. 4.3;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GKVAITG 14

|||||

Db 8 GKVAITG 15

Search completed: October 30, 2002, 15:48:59

Job time : 20 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 30, 2002, 15:45:40 ; Search time 12 seconds

(without alignments)
813.111 Million cell updates/sec

Title: US-09-910-033a-2

Perfect score: 252

Sequence: 1 MSNRLDGKVAITGTGIG.....NESKFGTGFVVDGGYTAQ 252

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	4.0	29	12AH_CLOSA	P21215 clostridium
2	9	3.6	289	YHDF_BACSU	Q07575 bacillus su
3	8	3.2	251	CHBR2_CAEEL	Q21929 caenorhabdi
4	8	3.2	276	1 DHCA_HUMAN	P16152 homo sapien
5	8	3.2	276	1 DHCA_RAT	P47727 rattus norv
6	8	3.2	307	1 YAC2_SCHPO	Q09816 schizosacch
7	8	3.2	336	1 TS2_MAIZE	P50160 zea mays (m
8	7	2.8	103	1 NTPG_ENTHR	P43455 enterococu
9	7	2.8	141	1 HBA_MUSPF	P20243 mustela put
10	7	2.8	141	1 HBA_SPECI	P09420 spermophili
11	7	2.8	141	1 BDA_SPEPA	P11750 spermophili
12	7	2.8	178	1 BDH_BOVIN	Q02337 bos taurus
13	7	2.8	205	1 VATO_HUMAN	Q99437 homo sapien
14	7	2.8	211	1 PCPI_SULSO	P58201 sulfolobus
15	7	2.8	228	1 FLPA_METVO	P35553 methanococ
16	7	2.8	241	1 BUDC_KLETE	Q04520 klebsiella
17	7	2.8	241	1 PHBB_RHIME	P50205 rhizobium m
18	7	2.8	241	1 PHBB_ZOORA	P23238 zoogloea ra
19	7	2.8	242	1 PHBG_HAEIN	P43713 haemophilus
20	7	2.8	242	1 MYF6_CHICK	Q01795 gallus gall
21	7	2.8	242	1 PHAB_PARDE	P50204 paracoccus
22	7	2.8	244	1 PHAB_ECOLI	P25716 escherichia
23	7	2.8	244	1 PHBG_SALTY	O85141 salmonella
24	7	2.8	244	1 PHBG_VIBCH	Q9K97 vibrio chol
25	7	2.8	244	1 PHBG_VIBHA	P55336 vibrio harv
26	7	2.8	245	1 NODG_RHIME	P72332 rhizobium m
27	7	2.8	245	1 NODG_RHIS3	P62334 rhizobium s
28	7	2.8	246	1 PHBG_BACSU	P51831 bacillus su
29	7	2.8	246	1 PHBG_THEMEA	O9X248 thermotoga
30	7	2.8	246	1 NODG_AZOR	P17611 azospirilli
31	7	2.8	247	1 PHBG_MYCTO	Q48930 mycobacteri
32	7	2.8	247	1 FAGI_SYNT3	P73574 synechocyst
33	7	2.8	247	1 YGFF_ECOLI	P52037 escherichia

34	7	2.8	248	1	FABG_AQUAE	O67610 aquifex ae
35	7	2.8	248	1	FABG_CHLPN	O928p2 chlamydia p
36	7	2.8	248	1	PHAB_ACISP	P50203 acinetobact
37	7	2.8	250	1	LINX_PSEPA	P50198 pseudomonas
38	7	2.8	251	1	Y325_THEMEA	O9W790 thermotoga
39	7	2.8	252	1	DLTE_BACSU	P39577 bacillus su
40	7	2.8	253	1	3BHD_COMTE	P19871 comamonas t
41	7	2.8	253	1	KDUD_ERWCH	O05528 erwinia chr
42	7	2.8	254	1	IDNO_ECOLI	P39345 escherichia
43	7	2.8	254	1	KDUD_BACSU	P50842 bacillus su
44	7	2.8	255	1	2BHD_STREX	P19992 streptomyce
45	7	2.8	255	1	FABG_MYCAV	O07399 mycobacteri

ALIGNMENTS

RESULT 1

12AH_CLOSA	STANDARD;	PRT;	29 AA.
ID	12AH_CLOSA		
AC	P21215;		
DT	01-AUG-1991 (Rel. 19, Created)		
DT	01-AUG-1991 (Rel. 19, Last sequence update)		
DT	01-AUG-1991 (Rel. 19, Last annotation update)		
DE	12-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.176) (Fragment).		
OS	Clostridium sp. (strain C 48-50).		
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;		
OC	Clostridium.		
OX	NCBI_TaxID=1507;		
RN	[1]		
RP	SEQUENCE.		
RA	MEDLINE-91177018; PubMed-2007406;		
RX	Braun M., Luensdorf H., Bueckmann A.F.;		
RT	*12 alpha-hydroxysteroid dehydrogenase from Clostridium group P,		
RT	strain C 48-50. Production, purification and characterization.*;		
RL	Eur. J. Biochem. 196:439-450(1991).		
CC	-!- FUNCTION: CATALYZES THE OXIDATION OF THE 12-ALPHA-HYDROXYL GROUP		
CC	OF BILE ACIDS, BOTH IN THEIR FREE AND CONJUGATED FORM. ALSO ACTS		
CC	ON BILE ALCOHOLS.		
CC	-!- CATALYTIC ACTIVITY: 3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-		
CC	cholanoate + NADP(+) = 3-alpha,7-alpha-dihydroxy-12-oxo-5-beta-		
CC	cholanoate + NADPH.		
CC	-!- SUBUNIT: HOMOTETRAMER.		
CC	-!- MISCELLANEOUS: THE THERMOSTABILITY OF THE ENZYME IS GREATLY		
CC	INCREASED DUE TO NADP BINDING.		
DR	PIR; SI4099; SI4099.		
KW	Oxidoreductase; NADP.		
FT	NON_TER 29		
SQ	SEQUENCE 29 AA; 2900 MW; A827DB34DB6C8812 CRC64;		

Query Match 4.0%; Score 10; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	6	DGKVAITGG 15	
DB	4	DGKVAITGG 13	

RESULT 2

YHDF_BACSU	STANDARD;	PRT;	289 AA.
ID	YHDF_BACSU		
AC	O07575;		
DT	15-JUL-1998 (Rel. 36, Created)		
DT	15-JUL-1998 (Rel. 36, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Hypothetical oxidoreductase yhdF (EC 1.-.-.-).		
GN	YHDF.		
OS	Bacillus subtilis.		
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;		
OC	Bacillus/Staphylococcus group; Bacillus.		
OX	NCBI_TaxID=1423;		
RN	[1]		

```

RP SEQUENCE FROM N.A.
RC STRAIN-168;
RA Noback M.A., Terpstra P., Holsappel S., Venema G., Bron S.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
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CC EMBL; Y14082; CAA74490.1;
CC EMBL; Z99109; CAB12784.1;
CC HSSP; P50162; IAE1.
CC Subtilist; BG13012; yhaF.
CC InterPro; IPR002198; ADH_short.
CC Pfam; PF00106; adh_short; 1.
CC PROSITE; PS00061; ADH_SHORT; 1.
CC KW Hypothetical protein; Oxidoreductase; Complete proteome.
CC FT NP_BIND 49 73 NAD OR NADP (BY SIMILARITY).
CC ACT_SITE 194 194 BY SIMILARITY.
CC SQ SEQUENCE 289 AA; 31509 MW; 4EC98C62B9241BC1 CRC64;

Query Match 3.6%; Score 9; DB 1; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GKVAITGG 15
DB 45 GKVAITGG 53

RESULT 3
CBB2_CABEL STANDARD; PRT; 251 AA.
AC Q21929;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Probable carbonyl reductase [NADPH] (EC 1.1.1.184) (NADPH-dependent
DE carbonyl reductase).
DS R1D1.11.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Steward C.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: R-CHOH-R' + NADP(+) -> R-CO-R' + NADPH (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC -----
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CC -----
CC EMBL; Z75547; CAA99897.1;
CC HSSP; P08074; LCYD.
CC WormPep; R1D1.11; CE06316.
CC InterPro; IPR002198; ADH_short.

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DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NADP; Mitochondrion.
FT NP_BIND 11 41 NADP (ADP RIBOSE PART) (BY SIMILARITY).
FT ACT_SITE 156 156 BY SIMILARITY.
FT DOMAIN 203 206 POLY-LYS.
SQ SEQUENCE 251 AA; 27188 MW; 4F51C9FA802D797D CRC64;

Query Match 3.2%; Score 8; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 LVNNAGIA 94
DB 87 LVNNAGIA 94

RESULT 4
DHCA_HUMAN STANDARD; PRT; 276 AA.
AC P16152;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Carbonyl reductase [NADPH] 1 (EC 1.1.1.184) (NADPH-dependent carbonyl
DE reductase 1) (Prostaglandin-E2 9-reductase) (EC 1.1.1.189)
DE (Prostaglandin 9-ketoreductase) (15-hydroxyprostaglandin dehydrogenase
DE [NADP+]) (EC 1.1.1.197).
DS CBRI OR CBR OR CRN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Placenta;
RC MEDLINE=89034082; PubMed=3141401;
RA Wermuth B., Bohren K.M., Heinemann G., von Wartburg J.-P.,
RA Gabbay K.H.;
RT "Human carbonyl reductase. Nucleotide sequence analysis of a cDNA and
RT amino acid sequence of the encoded protein."
RL J. Biol. Chem. 263:16185-16188(1988).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Breast;
RC MEDLINE=90212644; PubMed=2182121;
RA Forrest G.L., Akman S., Krutzik S., Paxton R.J., Sparkes R.S.,
RA Doroshov J., Felsted R.L., Mohandas T., Bachur N.R.;
RT "Induction of a human carbonyl reductase gene located on chromosome
RT 21."
RL Biochim. Biophys. Acta 1048:149-155(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=92017676; PubMed=1921984;
RA Forrest G.L., Akman S., Doroshov J., Rivera H., Kaplan W.D.;
RT "Genomic sequence and expression of a cloned human carbonyl reductase
RT gene with daunorubicin reductase activity."
RL Mol. Pharmacol. 40:502-507(1991).
RN [4]
RP SEQUENCE FROM N.A.
RC MEDLINE=98414514; PubMed=9740676;
RA Watanabe K., Sugawara C., Ono A., Fukuzumi Y., Itakura S.,
RA Yamazaki M., Tashiro H., Osoegawa K., Soeda E., Nomura T.;
RT "Mapping of a novel human carbonyl reductase, CBR3, and ribosomal
RT pseudogenes to human chromosome 21q22.2."
RL Genomics 52:95-100(1998).
RN [5]
RP SEQUENCE FROM N.A.
RA Shibuya K., Kudoh J., Minoshima S., Kawasaki K., Nakatoh E.,
RA Shintani A., Asakawa S., Shimizu N.;
RT "Genomic sequencing of 1.2-Mb region on human chromosome 21q22.2."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

```


[6]
RN RP SEQUENCE FROM N.A.
RX MEDLINE-20289793; PubMed-10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
RA Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhaber M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordstiek G., Hornischer K., Brandt P.,
RA Sharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,
RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Mizetic D., Francis F.,
RA Leinhardt H., Reinhardt R., Yaspo M.-L.;
RA "The DNA sequence of human chromosome 21.";
RL Nature 405:311-319(2000).
[7]
RN RP PARTIAL SEQUENCE, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE-93133816; PubMed-8421682;
RA Krook M., Ghosh D., Stromberg R., Carlquist M., Joernvall H.;
RA "Carboxyethyllysine in a protein: native carbonyl reductase/NADP(+)-
RT dependent prostaglandin dehydrogenase.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:502-506(1993).
CC -1- FUNCTION: CATALYZE THE REDUCTION OF A WIDE VARIETY OF CARBONYL
CC COMPOUNDS INCLUDING THE ANTITUMOR ANTHRACYCLINE ANTIBIOTICS.
CC CAN CONVERT PROSTAGLANDIN E2 TO PROSTAGLANDIN F2-ALPHA.
CC -1- CATALYTIC ACTIVITY: R-CHOH-R' + NADP(+) = R-CO-R' + NADPH.
CC -1- CATALYTIC ACTIVITY: (5Z,13E)-(15S)-9,11,15-trihydroxyprosta-5,13-
CC dienate + NADP(+) = (5Z,13E)-(15S)-11,15-dihydroxy-9-oxoprosta-
CC 5,13-dienate + NADPH.
CC -1- CATALYTIC ACTIVITY: (5Z,13E)-(15S)-11-alpha,15-dihydroxy-9-
CC oxoprosta-13-enate + NADP(+) = (5Z,13E)-11-alpha-hydroxy-9,15-
CC dihydroprosta-13-enate + NADPH.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
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CC EMBL: J04056; AAA52070.1; -;
CC EMBL: M62420; AAA1788.1; -;
CC EMBL: AB003351; BAA33498.1; -;
CC EMBL: AP000688; BAA89424.1; -;
CC EMBL: AP001724; BAA95508.1; -;
CC PIR: A31912; R0HUCB.
CC PIR: S09013; S09013.
CC HSP: P14061; IFDW.
CC MW: 114830; -;
CC InterPro: IPR002198; ADH_short.
CC Pfam: PF00106; adh_short; 1.
CC PRINTS: PR00081; GDRDH.
CC PROSITE: PS00061; ADH_SHORT; 1.
CC Oxidoreductase; NADP; Acetylation.
CC INIT_MET 0 0
CC MOD_RES 1 1 ACETYLATION.
CC NP_BIND 238 238 N6-(1-CARBOXYETHYL).
CC FT ACT_SITE 9 33 NADP (BY SIMILARITY).
CC FT ACT_SITE 193 193 BY SIMILARITY.
CC SQ SEQUENCE 276 AA; 30244 MW; 78E3065F5677733 CRC64;
Query Match 3.2%; Score 8; DB 1; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 87 LVNNAGIA 94

|||||||
DB 86 LVNNAGIA 93
RESULT 5
DHCA_RAT STANDARD; PRT; 276 AA.
ID AC P47727;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Carbonyl reductase [NADPH] 1 (EC 1.1.1.184) (NADPH-dependent carbonyl
DE reductase 1).
GN CBRI OR CBR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN RP SEQUENCE FROM N.A.
RX STRAIN-SPRAGUE-DAWLEY; TISSUE-Testis;
RA MEDLINE-95220378; PubMed-7705364;
RA Wermuth B., Maeder-Heinemann G., Ernst E.;
RA "Cloning and expression of carbonyl reductase from rat testis.";
RL Eur. J. Biochem. 228:473-479(1995).
CC -1- CATALYTIC ACTIVITY: R-CHOH-R' + NADP(+) = R-CO-R' + NADPH.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC
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CC
CC EMBL: X84349; CAA59088.1; -;
CC EMBL: X95986; CAA65230.1; -;
CC InterPro: IPR002198; ADH_short.
CC Pfam: PF00106; adh_short; 1.
CC PRINTS: PR00081; GDRDH.
CC PROSITE: PS00061; ADH_SHORT; 1.
CC Oxidoreductase; NADP; Acetylation.
CC INIT_MET 0 0 BY SIMILARITY.
CC MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
CC NP_BIND 9 33 NADP (BY SIMILARITY).
CC FT ACT_SITE 193 193 BY SIMILARITY.
CC SQ SEQUENCE 276 AA; 30447 MW; 99B9E77C5E2922AB CRC64;
Query Match 3.2%; Score 8; DB 1; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 87 LVNNAGIA 94
|||||||
DB 86 LVNNAGIA 93
RESULT 6
YAC2_SCHPO STANDARD; PRT; 307 AA.
ID AC Q09816;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 33.9 kDa protein C16C9.02C in chromosome 1.
GN SPAC16C9.02C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomyces.

OX NCBI_TaxID=4896;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RA Badcock K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;

RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE PNP/MTAP FAMILY 2 OF PHOSPHORYLASES.

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CC -----

DR EMBL: Z54366; CAA91190.1; -

DR HSP; Q13126; ICB0.

DR InterPro: IPR001369; Mtap_PNP.

DR Pfam: PF00896; Mtap_PNP; 1.

DR PROSITE: PS01240; PNP_MTPAP.2; 1.

KW Hypothetical protein; Transferase; Glycosyltransferase.

SQ SEQUENCE 307 AA; 33847 MW; A289285BFD438067 CRC64;

Query Match

Best Local Similarity 3.2%; Score 8; DB 1; Length 307;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 135 GASTINMS 142

DB | | | | |

DB 192 GASTINMS 199

RESULT 7

TS2_MAIZE

ID TS2_MAIZE STANDARD; PRT; 336 AA.

AC P50160;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Sex determination protein tasselseed 2.

GN TS2.

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;

OC Panicoideae; Andropogoneae; Zea.

OX NCBI_TaxID=4577;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=CV. W22;

RX MEDLINE=93364991; PubMed=8358795;

RA DeLong A., Calderon-Urrea A., Dellaporta S.L.;

RT Sex determination gene TASSLSEED2 of maize encodes a short-chain

RT alcohol dehydrogenase required for stage-specific floral organ

RT abortion.;

RL Call 74:757-768(1993).

CC -1- FUNCTION: REQUIRED FOR STAGE-SPECIFIC FLORAL ORGAN ABORTION.

CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES

CC (SDR) FAMILY.

CC -----

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CC -----

DR EMBL: L20621; AAC37345.1; -

DR HSP; P19992; IHDC.

DR MaizeDB; 56963; -

DR InterPro: IPR002198; ADH_short.

DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Oxidoreductase; Developmental protein.
FT NP_BIND 59 83
FT ACT_SITE 207 207 BY SIMILARITY.
SQ SEQUENCE 336 AA; 35204 MW; 4E273D6152B0BB99 CRC64;

Query Match

Best Local Similarity 3.2%; Score 8; DB 1; Length 336;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 RLDGKVAI 11

DB | | | | |

DB 52 RLDGKVAI 59

RESULT 8

NTPG_ENTHR

ID NTPG_ENTHR STANDARD; PRT; 103 AA.

AC P43455;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE V-type sodium ATP synthase subunit G (EC 3.6.3.14) (Na(+)-

DE translocating ATPase subunit G).

GN NTPG OR NTPQ.

OS Enterococcus hirae.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;

OC Enterococcus.

OX NCBI_TaxID=1354;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN-ATCC 9790;

RX MEDLINE=94209269; PubMed=8157629;

RA Takase K., Kakinuma S., Yamato I., Konishi K., Igarashi K.,

RA Kakinuma Y.;

RT "Sequencing and characterization of the ntp gene cluster for

RT vacuolar-type Na(+)-translocating ATPase of Enterococcus hirae.;"

RL J. Biol. Chem. 269:11037-11044(1994).

RN (2)

RP SEQUENCE FROM N.A.

RC STRAIN-ATCC 9790;

RX MEDLINE=94193617; PubMed=8144530;

RA Solioz M., Davies K.;

RT "Operon of vacuolar-type Na(+)-ATPase of Enterococcus hirae.;"

RL J. Biol. Chem. 269:9453-9459(1994).

CC -1- FUNCTION: INVOLVED IN ATP-DRIVEN SODIUM EXTRUSION.

CC -1- SIMILARITY: BELONGS TO THE V-ATPASE F SUBUNIT FAMILY.

CC -----

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CC -----

DR EMBL: D17462; BAA04274.1; -

DR EMBL; X76913; CAA54240.1; -

DR InterPro: IPR002841; ATP-synt_F.

DR Pfam: PF01990; ATP-synt_F; 1.

DR Propom; PD003811; ATP-synt_F; 1.

KW Hydrolase; ATP synthetis; Hydrogen ion transport.

SQ SEQUENCE 103 AA; 11410 MW; 5F452721633D3960 CRC64;

Query Match

Best Local Similarity 2.8%; Score 7; DB 1; Length 103;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 GTLIGL 21

DB | | | | |

DB 81 GTLIGL 87

DR PRINTS; PR00612; ALPHAHAE. 2.8%; Score 7; DB 1; Length 141; Indels 0; Gaps 0;
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transprot; Erythrocyte.
FT METAL 58 58 IRON (HEME DISTAL LIGAND).
FT METAL 87 87 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 141 AA; 15192 MW; 365EA7E98227347B CRC64;
Query Match 2.8%; Score 7; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 196 VDDLPGA 202
Db 73 VDDLPGA 79
RESULT 11
HBA_SPEA STANDARD; PRT; 141 AA.
ID HBA_SPEA P11750;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Hemoglobin alpha chain.
OS Sperophilus parvii (Arctic ground squirrel) (Citellus parryi).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Sperophilus
OX NCBI_TaxID=9999;
RN [1]
RP SEQUENCE.
RX MEDLINE=87274834; PubMed=3608432;
RA Duffy L.K., Ehrhardt M.M., Genaux C.T., Florant G.L.;
RT "The primary structure of the hemoglobin alpha-chain of the arctic
ground squirrel";
RL Comp. Biochem. Physiol. 87B:189-193(1987).
DR PIR; J0165; J0165.
DR HSSP; P01922; 1B20.
DR InterPro; IPR002338; Alpha_haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00612; ALPHAHAE.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transprot; Erythrocyte;
FT METAL 58 58 IRON (HEME DISTAL LIGAND).
FT METAL 87 87 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 141 AA; 15047 MW; FF0D9DF6552D1F72 CRC64;
Query Match 2.8%; Score 7; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 196 VDDLPGA 202
Db 73 VDDLPGA 79
RESULT 12
BDH_BOVIN STANDARD; PRT; 178 AA.
ID BDH_BOVIN Q02337;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE D-beta-hydroxybutyrate dehydrogenase (EC 1.1.1.30) (BDH)
DE (3-hydroxybutyrate dehydrogenase) (Fragments).
GN BDH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]

DR PRINTS; PR00612; ALPHAHAE. 2.8%; Score 7; DB 1; Length 141; Indels 0; Gaps 0;
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transprot; Erythrocyte.
FT METAL 58 58 IRON (HEME DISTAL LIGAND).
FT METAL 87 87 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 141 AA; 15192 MW; 365EA7E98227347B CRC64;
Query Match 2.8%; Score 7; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 196 VDDLPGA 202
Db 73 VDDLPGA 79
RESULT 11
HBA_SPEA STANDARD; PRT; 141 AA.
ID HBA_SPEA P11750;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Hemoglobin alpha chain.
OS Sperophilus parvii (Arctic ground squirrel) (Citellus parryi).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Sperophilus
OX NCBI_TaxID=9999;
RN [1]
RP SEQUENCE.
RX MEDLINE=87274834; PubMed=3608432;
RA Duffy L.K., Ehrhardt M.M., Genaux C.T., Florant G.L.;
RT "The primary structure of the hemoglobin alpha-chain of the arctic
ground squirrel";
RL Comp. Biochem. Physiol. 87B:189-193(1987).
DR PIR; J0165; J0165.
DR HSSP; P01922; 1B20.
DR InterPro; IPR002338; Alpha_haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00612; ALPHAHAE.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transprot; Erythrocyte;
FT METAL 58 58 IRON (HEME DISTAL LIGAND).
FT METAL 87 87 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 141 AA; 15047 MW; FF0D9DF6552D1F72 CRC64;
Query Match 2.8%; Score 7; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 196 VDDLPGA 202
Db 73 VDDLPGA 79
RESULT 12
BDH_BOVIN STANDARD; PRT; 178 AA.
ID BDH_BOVIN Q02337;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE D-beta-hydroxybutyrate dehydrogenase (EC 1.1.1.30) (BDH)
DE (3-hydroxybutyrate dehydrogenase) (Fragments).
GN BDH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]

DR PRINTS; PR00612; ALPHAHAE. 2.8%; Score 7; DB 1; Length 141; Indels 0; Gaps 0;
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transprot; Erythrocyte.
FT METAL 58 58 IRON (HEME DISTAL LIGAND).
FT METAL 87 87 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 141 AA; 15192 MW; 365EA7E98227347B CRC64;
Query Match 2.8%; Score 7; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 196 VDDLPGA 202
Db 73 VDDLPGA 79
RESULT 11
HBA_SPEA STANDARD; PRT; 141 AA.
ID HBA_SPEA P11750;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Hemoglobin alpha chain.
OS Sperophilus parvii (Arctic ground squirrel) (Citellus parryi).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Sperophilus
OX NCBI_TaxID=9999;
RN [1]
RP SEQUENCE.
RX MEDLINE=87274834; PubMed=3608432;
RA Duffy L.K., Ehrhardt M.M., Genaux C.T., Florant G.L.;
RT "The primary structure of the hemoglobin alpha-chain of the arctic
ground squirrel";
RL Comp. Biochem. Physiol. 87B:189-193(1987).
DR PIR; J0165; J0165.
DR HSSP; P01922; 1B20.
DR InterPro; IPR002338; Alpha_haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00612; ALPHAHAE.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transprot; Erythrocyte;
FT METAL 58 58 IRON (HEME DISTAL LIGAND).
FT METAL 87 87 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 141 AA; 15047 MW; FF0D9DF6552D1F72 CRC64;
Query Match 2.8%; Score 7; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 196 VDDLPGA 202
Db 73 VDDLPGA 79
RESULT 12
BDH_BOVIN STANDARD; PRT; 178 AA.
ID BDH_BOVIN Q02337;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE D-beta-hydroxybutyrate dehydrogenase (EC 1.1.1.30) (BDH)
DE (3-hydroxybutyrate dehydrogenase) (Fragments).
GN BDH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]

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DR EMBL; AE006762; AAK41693.1; ..
DR InterPro; IPR000816; Peptidase_C15.
DR Pfam; PF01470; Peptidase_C15; 1.
DR ProDom; PD008480; Peptidase_C15; 1.
DR PROSITE; PS01333; PYRASE_GLU; 1.
DR PROSITE; PS01334; PYRASE_CYS; 1.
KW Hydrolase; Thiol protease; Complete proteome.
FT ACT_SITE 79 79 BY SIMILARITY.
FT ACT_SITE 142 142 BY SIMILARITY.
FT ACT_SITE 164 164 BY SIMILARITY.
SQ SEQUENCE 211 AA; 23680 MW; 84416BE3CB745AB4 CRC64;

Query Match 2.8%; Score 7; DB 1; Length 211;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 TLGIGLA 22
|||||
DB 64 TLGIGLA 70

RESULT 15

FLPA_METVO
ID FLPA_METVO STANDARD; PRT; 228 AA.
AC P35553;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Fibrillarlin-like pre-rRNA processing protein.
GN FLPA OR RPPA.
OS Methanococcus voltae.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2188;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1537 / PS;
RX MEDLINE=94193565; PubMed=8144483;
RA Agha Amir K.;
RT "Fibrillarlin-like proteins occur in the domain Archaea.";
RL J. Bacteriol. 176:2124-2127(1994).
CC -!- FUNCTION: MAY BE INVOLVED IN PRE-RRNA PROCESSING.
CC -!- SIMILARITY: BELONGS TO THE FIBRILLARIN FAMILY.
CC
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DR EMBL; X73988; CAA52166.1; ..
DR PIR; S34646; S34646.
DR HSP; Q58108; 1FBN.
DR InterPro; IPR000692; Fibrillarlin.
DR Pfam; PF01269; Fibrillarlin; 1.
DR PRINTS; PR00052; FIBRILLARIN.
DR ProDom; PD004637; Fibrillarlin; 1.
DR PROSITE; PS00566; FIBRILLARIN; 1.
KW rRNA processing; rRNA-binding.
SQ SEQUENCE 228 AA; 25618 MW; 0AB2418DE0E324CF CRC64;

Query Match 2.8%; Score 7; DB 1; Length 228;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 134 LGASIIN 140
|||||

Db 57 LGASIIN 63

Search completed: October 30, 2002, 15:47:21
Job time : 13 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	12	4.8		273	10	Q9SBM0	Q9sbm0 citrullus l
2	10	4.0		247	2	Q93RM0	Q93rm0 acinetobact
3	10	4.0		251	2	Q9F7E0	Q9f7e0 acinetobact
4	10	4.0		260	16	Q9A326	Q9a326 caulobacter
5	9	3.6		250	5	O17721	O17721 caenorhabdi
6	9	3.6		267	10	P93697	P93697 vigna ungui
7	9	3.6		283	16	Q9A4H3	Q9a4h3 caulobacter
8	9	3.6		303	10	Q9SCU0	Q9scu0 arabidopsis
9	8	3.2		65	6	Q9TSA9	Q9tsa9 sus scrofa
10	8	3.2		65	6	Q9TSA2	Q9tsa2 sus scrofa
11	8	3.2		161	10	Q9LL33	Q9ll33 lycopersico
12	8	3.2		238	16	Q9HWL9	Q9hw19 pseudomonas
13	8	3.2		249	2	Q96841	Q96841 xanthobacte
14	8	3.2		250	2	Q93714	Q93714 comamonas t
15	8	3.2		251	10	Q40133	Q40133 lycopersico
16	8	3.2		251	16	Q98H76	Q98h76 rhizobium l

12 RUDGKVALTGG 23

4 RLDGKVAITGG 15
|||||
12 RLDGKVAITGG 23

```

RESULT 2
Q93RMO PRELIMINARY; PRT; 247 AA.
ID AC Q93RMO;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE DE CYCLOHEXANOL DEHYDROGENASE.
GN CHNA.
OS Acinetobacter sp. NCIMB9871.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC Acinetobacter.
OX NCBI_TaxID=93373;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 9871;
RA Iwaki H., Hasegawa Y., Teraoka M., Tokuyama T., Lau P.C.;
RT "Identification and Characterization of Cyclohexanol Metabolic Genes
from Acinetobacter sp. NCIMB 9871.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB026668; BAB61742.1;
SQ SEQUENCE 247 AA; 25657 MW; AB0DA7904DE726B3 CRC64;

Query Match 4.0%; Score 10; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 186 VHPGYIKTPL 195
| | | | | | | |
DB 185 VHPGYIKTPL 194

RESULT 3
Q9F7E0 PRELIMINARY; PRT; 251 AA.
ID AC Q9F7E0;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE DE CYCLOHEXANOL DEHYDROGENASE.
GN CHNA.
OS Acinetobacter sp. SE19.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC Acinetobacter.
OX NCBI_TaxID=135835;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SE19;
RA Cheng Q., Thomas S.M., Kostichka K., Nagarajan V.;
RT "Genetic analysis of a gene cluster for cyclohexanol oxidation in
acinetobacter sp. strain SE19 by in vitro transposition.";
RL J. Bacteriol. 182:4744-4751(2000).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
DR EMBL; AF282240; AAG10026.1;
DR HSSP; P19992; IHDC.
DR InterPro; IPR002198; ADH_short.
DR PRINTS; PR00080; SDRFAMILY.
KW Oxidoreductase.
SQ SEQUENCE 251 AA; 26159 MW; B5BAA48055997D5D CRC64;

Query Match 4.0%; Score 10; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 186 VHPGYIKTPL 195
| | | | | | | |
DB 189 VHPGYIKTPL 198

RESULT 4

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Q9A326 PRELIMINARY; PRT; 260 AA.
ID AC Q9A326;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE DE 2-DEOXY-D-GLUCONATE 3-DEHYDROGENASE.
GN CC3380.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=69394;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RA MEDLINE=21173698; PubMed=11259647;
RA Nieman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potočka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Uterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
DR EMBL; AE005999; AAK25342.1;
DR HSSP; P19992; IHDC.
DR TIGR; CC3380;
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
KW Complete proteome; Oxidoreductase.
SQ SEQUENCE 260 AA; 26992 MW; 96B83C46AB23E805 CRC64;

Query Match 4.0%; Score 10; DB 16; Length 260;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 LAVNLGCVFF 120
| | | | | | | |
DB 116 LAVNLGCVFF 125

RESULT 5
Q17721 PRELIMINARY; PRT; 250 AA.
ID AC Q17721;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE DE C55A6.6 PROTEIN.
GN C55A6.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Kerahaw J.K.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
investigating biology.";
RL Science 282:2012-2018(1998).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
DR EMBL; Z81051; CAB02866.1;

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DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
KW Oxidoreductase.
SQ SEQUENCE 250 AA; 27060 MW; 95A2C768163B82CE CRC64;
Query Match 3.6%; Score 9; DB 5; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 87 LVNAGIAY 95
| | | | | | | | | |
DB 85 LVNAGIAY 93

RESULT 6
P93697 PRELIMINARY; PRT; 267 AA.
AC P93697;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CPRO12 PROTEIN.
OS Vigna unguiculata (Cowpea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3917;
RN [1]
RP SEQUENCE FROM N.A.
RA Iuchi S., Yamaguchi-Shinozaki K., Urao T., Shinozaki K.;
RT "Characterization of two cDNAs for novel drought-inducible genes in
RT the highly drought-tolerant cowpea.";
RL J. Plant Res. 109:415-424(1996).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL: D88121; DAA13541.1; -;
DR HSSP: P19992; IHDC.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.
KW Oxidoreductase.
SQ SEQUENCE 267 AA; 28484 MW; 8C4A8A2E9F41B64 CRC64;
Query Match 3.6%; Score 9; DB 10; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 GKVAITGG 15
| | | | | | | | | |
DB 16 GKVAITGG 24

RESULT 7
O9A4H3 PRELIMINARY; PRT; 283 AA.
ID O9A4H3;
AC O9A4H3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE OXIDOREDUCTASE, SHORT-CHAIN DEHYDROGENASE/REDUCTASE FAMILY.
GN CC2861.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=69394;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Taub M.T., Paulsen I.T., Nelson K.E.,
RA Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton C., Stephens C., Phadke N.D., Ely B.,


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DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE PROSTAGLANDIN 9-KETOREDUCTASE (EC 1.1.1.189) (FRAGMENTS).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1];
RP SEQUENCE.
RX MEDLINE=92283276; PubMed=1597188;
RA Schieber A., Frank R.W., Ghisla S.;
RT "Purification and properties of prostaglandin 9-ketoreductase from pig
and human kidney. Identity with human carbonyl reductase."
RL Eur. J. Biochem. 206:491-502(1992).
FT NON_TER 1 1
FT NON_CONS 15 16
FT NON_CONS 30 31
FT NON_CONS 45 46
FT NON_CONS 56 57
FT NON_TER 65 65
SQ SEQUENCE 65 AA; 6922 MW; E821D57EE2001FAE CRC64;

Query Match 3.2%; Score 8; DB 6; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 LVNNAGIA 94
Db 8 LVNNAGIA 15

RESULT 10
Q9TSA2
ID Q9TSA2 PRELIMINARY; PRT; 65 AA.
AC Q9TSA2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE PROSTAGLANDIN 9-KETOREDUCTASE (EC 1.1.1.184) (FRAGMENTS).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1];
RP SEQUENCE.
RX MEDLINE=93081046; PubMed=1449827;
RA Schieber A., Ghisla S.;
RT "Prostaglandin 9-ketoreductase from pig and human kidney:
purification, properties and identity with human carbonyl reductase."
RL Eicosanoids 5:37-37(1992).
FT NON_TER 1 1
FT NON_CONS 15 16
FT NON_CONS 30 31
FT NON_CONS 45 46
FT NON_CONS 56 57
FT NON_TER 65 65
SQ SEQUENCE 65 AA; 6934 MW; 462F257EE2001FB2 CRC64;

Query Match 3.2%; Score 8; DB 6; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 LVNNAGIA 94
Db 8 LVNNAGIA 15

RESULT 11
Q9LL33
ID Q9LL33 PRELIMINARY; PRT; 161 AA.
AC Q9LL33;
DT 01-OCT-2000 (Tremblrel. 15, Created)

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DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE LIGHT DEPENDENT NADH:PROTOCHLOROPHYLLIDE OXIDOREDUCTASE 3
DE (FRAGMENT).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1];
RP SEQUENCE FROM N.A.
RA Rubiera R., Neuhaus G.;
RT "Cloning of three putative light-dependent NADH:protochlorophyllide
oxidoreductases from Lycopersicon esculentum."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF243524; AAF82474.1;
FT NON_TER 1 1
FT NON_TER 161 161
SQ SEQUENCE 161 AA; 17286 MW; 5D1AB2EF071DBC6D CRC64;

Query Match 3.2%; Score 8; DB 10; Length 161;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 EKAASVG 52
Db 7 EKAASVG 14

RESULT 12
Q9HML9
ID Q9HML9 PRELIMINARY; PRT; 238 AA.
AC Q9HML9;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE PROBABLE SHORT-CHAIN DEHYDROGENASE.
GN PA4162.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1];
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen."
RL Nature 406:959-964(2000).
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY
DR EMBL; AE004832; AAG07549.1;
DR HSSP; P50162; LAEI.
DR InterPro; IPR002198; ADH_short.
DR PRINTS; PRO0080; SDRFAMILY.
KW Complete proteome; Oxidoreductase.
SQ SEQUENCE 238 AA; 24857 MW; 34643FA76B2B44CD CRC64;

Query Match 3.2%; Score 8; DB 16; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 LVNNAGIA 94
Db 73 LVNNAGIA 80

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RESULT 13

Q56841 PRELIMINARY; PRT; 249 AA.
 AC Q56841;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ORF5 PROTEIN.
 GN ORF5.
 OS Xanthobacter sp.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Hypnomicrobium group; Xanthobacter.
 OX NCBI_TaxID=35809;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PY2;
 RX MEDLINE=95219103; PubMed=7704278;
 RA Swaving J., Weljers C.A.G.M., van Ooyen A.J.J., de Bont J.A.M.;
 RT "Complementation of Xanthobacter Py2 mutants in epoxyalkane
 degradation: expression and nucleotide sequence of the complementing
 DNA fragment.";
 RT Microbiology 141:477-484(1995).
 RL -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY:
 CC EMBL; X79863; CAA56245.1; -;
 DR HSSP; P19992; IHDC.
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
 KW Oxidoreductase.
 SQ SEQUENCE 249 AA; 24940 MW; B5E0B82C1D8D9782 CRC64;

Query Match 3.2%; Score 8; DB 2; Length 249;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 LVNNAGIA 94
 DB 82 LVNNAGIA 89
 |||||

RESULT 14

Q937L4 PRELIMINARY; PRT; 250 AA.
 AC Q937L4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE CYCLOHEXANOL DEHYDROGENASE (EC 1.1.1.1).
 GN CPMB.
 OS Comamonas testosteroni (Pseudomonas testosteroni).
 OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
 OX NCBI_TaxID=285;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NCIMB 9872;
 RA van Beilen J.B., Fritsche U., Seeger M., Smits T.H.M., Witholt B.;
 RT "Cloning of Baeyer-Villiger monooxygenases from Comamonas,
 Xanthobacter and Rhodococcus via PCR with highly degenerate primers.";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ418060; CAD10799.1; -;
 KW Oxidoreductase.
 SQ SEQUENCE 250 AA; 26626 MW; 7C42C3CBAEBB858E CRC64;

Query Match 3.2%; Score 8; DB 2; Length 250;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 VVDGGYTA 251
 DB 242 VVDGGYTA 249
 |||||

RESULT 15

Q40133 PRELIMINARY; PRT; 251 AA.
 AC Q40133;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ALCOHOL DEHYDROGENASE HOMOLOG (FRAGMENT).
 GN GAD3.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. MONEYMAKER;
 RX MEDLINE=96158488; PubMed=8580773;
 RA Jacobsen S.E., Olszewski N.E.;
 RT "Gibberellins regulate the abundance of RNAs with sequence similarity
 to proteinase inhibitors, dioxigenases and dehydrogenases.";
 RL Planta 198:78-86(1996).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY:
 CC EMBL; U21801; AAB00109.1; -;
 DR HSSP; P29132; 1DFI.
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 KW Oxidoreductase.
 FT NON_TER 1
 SQ SEQUENCE 251 AA; 26202 MW; 8A6BCBDA15B90D53 CRC64;

Query Match 3.2%; Score 8; DB 10; Length 251;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GKVAIITG 14
 DB 2 GKVAIITG 9
 |||||

Search completed: October 30, 2002, 15:48:34
 Job time : 29 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 30, 2002, 15:45:05 ; Search time 20 Seconds
(without alignments)
1210.726 Million cell updates/sec

Title: US-09-910-033A-2
Perfect score: 1290
Sequence: I MSNLDGKVAITGGTIGIG.....NESKATGSEFVVDGGYTAQ 252

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB	ID	Description
1	470	36.4	261	2	E87279	hypothetical prote
2	464.5	36.0	260	2	H70758	probable fabG3 pro
3	407.5	31.6	255	1	S10707	20beta-hydroxyster
4	400.5	31.0	255	1	S39737	glucose 1-dehydrog
5	393	30.5	254	2	S48129	3(or 17)beta-hydro
6	391	30.3	249	2	S47055	hypothetical prote
7	383	29.7	256	2	E72427	oxidoreductase, sh
8	380	29.5	247	2	E70740	probable fabG2 pro
9	374.5	29.0	248	2	F69868	glucose 1-dehydrog
10	372.5	28.9	253	2	B95284	probable [imported
11	371.5	28.8	261	2	J50385	glucose 1-dehydrog
12	370.5	28.7	261	2	A33528	glucose 1-dehydrog
13	368	28.5	253	2	B86737	acetoin dehydrogen
14	367	28.4	258	2	C70885	probable dehydroge
15	366	28.4	272	2	A59950	hypothetical prote
16	365.5	28.3	246	2	H72219	3-oxoacyl-(acyl ca
17	365.5	28.3	263	2	S01227	glucose 1-dehydrog
18	364.5	28.3	255	2	D70635	hypothetical prote
19	363.5	28.2	261	1	S00812	glucose 1-dehydrog
20	363	28.1	262	2	S02299	glucose 1-dehydrog
21	359	27.8	254	2	AD3182	short chain dehydr
22	358.5	27.8	261	2	D69629	glucose 1-dehydrog
23	357.5	27.7	251	2	A13185	dehydrogenase Atu5
24	357.5	27.7	258	2	D95284	probable [imported
25	357.5	27.7	261	2	I40225	glucose 1-dehydrog
26	357.5	27.7	271	2	AC0157	probable short cha
27	357	27.7	296	2	E87260	hypothetical prote
28	356.5	27.6	248	2	H98258	3-oxoacyl-(acyl-ca
29	356.5	27.6	248	2	A13025	3-oxoacyl-(acyl-ca

30	355.5	27.6	261	2	I39853	glucose 1-dehydrog
31	352.5	27.3	261	2	I40224	glucose 1-dehydrog
32	351.5	27.2	251	2	G72389	oxidoreductase, sh
33	351	27.2	286	2	G83378	probable short-cha
34	350	27.1	257	2	A72395	oxidoreductase, sh
35	348.5	27.0	258	2	G69755	glucose 1-dehydrog
36	347	26.9	243	2	F83838	oxidoreductase (sh
37	346.5	26.9	255	2	D72377	oxidoreductase, sh
38	346	26.8	248	2	T44361	acetateacetyl-CoA re
39	346	26.8	267	2	AP2362	hypothetical prote
40	344	26.7	303	2	T46064	short-chain alchoho
41	343.5	26.6	250	1	S47054	probable dehydroge
42	343.5	26.6	299	2	D90481	hypothetical prote
43	342.5	26.6	267	2	T11579	probable short cha
44	342	26.5	253	2	T36782	probable gluconate
45	340	26.4	241	2	A12916	acetoacetyl CoA re

ALIGNMENTS

RESULT 1

E87279

hypothetical protein CC0246 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001

C:Accession: E87279

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; deBooy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kiro, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: E87279

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-261 <STO>

A:Cross-references: GB:AE005673; NID:g13421377; PIDN:ANK22233.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC0246

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 36.4%; Score 470; DB 2; Length 261;

Best Local Similarity 40.7%; Pred No. 4, 1e-30;

Matches 107; Conservative 46; Mismatches 90; Indels 20; Gaps 6;

OY 2 SNRLDGKVAITGGTIGIGLAITATKFEVGEAKVMTDRHSVDYGEKAASVGTDPDQIQ---58

Db 5 TGRVAGKKAFTGGAGGLGAAAGRLAKEGAKVAL---ADINLAGAQAQA--DEINAAH 58

OY 59 -----FQHDSSDEGWTKLEDATEKAFGPVSTLVNAGIAVKNKSVETTTAEWRKLLA 112

Db 59 GAGTAFAPFELDTQEDQWIDVLEKATAAAGGLSVLVNAGIGDGPISLDFGLMKKVM 118

OY 113 VNLDGVFFCTRLIGIORMKNKGLGASIIINSSIEGFGVDPISLGYNASKAGVIMSKSAAL 172

Db 119 VNVDVSLGAKHALTHMAHQPG-SIINLSSTAGLIANGSNPAYNASKAAVLLSKNIAL 177

OY 173 DCALKDYDVRVNTVHPGVIKTPLVDDLP---GAERAMSORTK-TPMGHIGEPNDIAYICV 228

Db 178 YCAKMKLDIRSNSIHPTFTDTPILDFGFSARFGKEAFARQVPLGRIGETPDIANAVL 237

OY 229 YLANSKFAFGSEFVVDGGYTA 251

Db 238 YLANSKFAFGSEFVVDGGYTA 260

RESULT 2

H70758

probable fabG3 protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C:Accession: H70758

R: Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M. A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
 A: Authors: Soares, R.; Sulston, J. E.; Taylor, K.; Whitehead, S.; Barrall, B. G.
 A: Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
 A: Reference number: A70500; MUID: 98295987
 A: Accession: H70758
 A: Status: preliminary; nucleic acid sequence not shown; translation not shown
 A: Molecule type: DNA
 A: Residues: 1-260 <COL>
 A: Cross-references: GB:Z74025; GB:AL123456; NID: g3261586; PIDN: CAA98414.1; PID: g3261591
 A: Experimental source: strain H37RV
 C: Genetics:
 C: Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 F: 8-184/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 36.0%; Score 464.5; DB 2; Length 260;
 Best Local Similarity 42.2%; Pred. No. 1.1e-29;
 Matches 106; Conservative 44; Mismatches 90; Indels 11; Gaps 5;

QY 1 MSNRLDGKVAITGGTGLGATATKFFVEGAKVMTDRHSDVGEKAASVGTDPQIQFF 60
 DB 1 MSGRLLGKVALVSGGARGMGASHVRAWAGKVFGLDDEGKAAVAAELA--DAARYV 58
 QY 61 QHDSDEDEGWTKLFDATKAFGVPSTLVNAGIAVKNKSVETTTAEWRKLLAVNLGCVFF 120
 DB 59 HLDVTPQAQWTAADVATVAFGLHVLVNNAGILNTIGTIEDYALTEWQRIIDVNLGCVFL 118

QY 121 GTRLGTRQMKNGKLGASIIINSSIEGFGVDPGSLGAYNASKGAVRIMSKSAALCALDKYD 180
 DB 119 GIRAVYKPKKEARG--SIINISIEGLAGTAVACHGYTATKFAVRGLTKSTALE--LGP 175

QY 181 VRVNTVHPCYIKTLPVDDLPGEAAMSQRTKTPMGHIGPNDIATYICVYLASNESKATG 240
 DB 176 IRVNSHRLGLVTPWTDVNP--EDIF----QALGRAAEPEVSNLVVILASDESISTG 229

QY 241 SEFVVDGGYTA 251
 DB 230 AEFVVDGGTVA 240

RESULT 3
 S10707
 20beta-hydroxysteroid dehydrogenase (EC 1.1.1.-) - *Streptomyces exfoliatus*
 C: Species: *Streptomyces exfoliatus*
 C: Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C: Accession: S10707

R: Marekov, L.; Krook, M.; Joernvall, H. FEBS Lett. 266, 51-54, 1990
 A: Title: Prokaryotic 20-beta-hydroxysteroid dehydrogenase is an enzyme of the 'short-chain' alcohol dehydrogenase family
 A: Reference number: S10707; MUID: 90306362
 A: Accession: S10707

A: Status: preliminary
 A: Molecule type: protein
 A: Residues: 1-255 <MAK>
 C: Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 F: 7-183/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 31.6%; Score 407.5; DB 1; Length 255;
 Best Local Similarity 39.0%; Pred. No. 3.8e-25;
 Matches 97; Conservative 42; Mismatches 103; Indels 7; Gaps 5;

QY 3 NRLDGKVAITGGTGLGATATKFFVEGAKVMTDRHSDVGEKAASVGTDPQIQFF 62
 DB 2 NDLGKVTIITGGTGLGAEAAQAAVAVLADVDEGAATARELG--DAARYQHL 59

QY 63 DSDSDEDEGWTKLFDATKAFGVPSTLVNAGIAVKNKSVETTTAEWRKLLAVNLGCVFF 120
 DB 60 DVTIEDQRVVAAREEFGVDGLVNNAGISTGMFETSEVERFRKYVDINLTGVTIGM 119

QY 123 RLGIQRMKNKGLGASIIINSSIEGFGVDPGSLGAYNASKGAVRIMSKSAALCALDKYDVR 182
 DB 120 KTVIPAMKDG--GGSIVNISSAAGLGLATSSYGASKWGVGLSKLAAYE--LCTDRIR 176
 QY 183 VNTVHPCYIKTLPVDDLPGEAAMSQRTKTPMGHIG--EPNDIATYICVYLASNESKATG 241
 DB 177 VNSVHPCYIKTLPVDDLPGEAAMSQRTKTPMGHIG--EPNDIATYICVYLASNESKATG 235
 QY 242 EFWVDGGYT 250
 DB 236 ELAVDGGWT 244

RESULT 4
 S39737
 glucose 1-dehydrogenase homolog ywfD - *Bacillus subtilis*
 N: Alternate names: protein ipa-82d
 N: Contains: probable dehydrogenase (EC 1.1.1.-)
 C: Species: *Bacillus subtilis*
 C: Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
 C: Accession: S39737; E70055
 R: Glaser, P.; Kunst, F.; Arnaud, M.; Coudart, M. P.; Gonzales, W.; Hullo, M. F.; Ionec, A.; Rapoport, G.; Danchin, A. Mol. Microbiol. 10, 371-384, 1993
 A: Title: *Bacillus subtilis* genome project: cloning and sequencing of the 97 kb regic
 A: Reference number: S39655; MUID: 95020537
 A: Accession: S39737
 A: Status: preliminary; nucleic acid sequence not shown; translation not shown
 A: Molecule type: DNA
 A: Residues: 1-255 <GLA>
 A: Cross-references: EMBL: X73124; NID: g413923; PIDN: CAA51638.1; PID: g414006
 A: Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1993
 R: Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A. M.; Alloni, G.; Azevedo, V.; Beron, S.; Brouillet, S.; Brusch, C. V.; Caldwell, B.; Capuano, V.; Carter, N. M.; A.; Ehrlich, S. D.; Emmerison, P. F.; Entian, K. D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
 A: Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Geiech, J.; Harwood, C. R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardir, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S. M.; Levine, A.; Liu, H.; Masuda, S.; Ma, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S. H.; Parro, V.; Pohl, T. M.; Portet, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scan, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sakeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiy, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshic, A.; Authors: Yoshikawa, H. F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A. *Bacillus subtilis*
 A: Title: The complete genome sequence of the Gram-positive bacterium
 A: Reference number: A69580; MUID: 98044033
 A: Accession: E70055
 A: Status: preliminary; nucleic acid sequence not shown; translation not shown
 A: Molecule type: DNA
 A: Residues: 1-255 <KUN>
 A: Cross-references: GB: Z99123; GB: AL009126; NID: g2636240; PIDN: CAB15799.1; PID: g2636

A: Experimental source: strain 168
 C: Genetics:
 C: Gene: ywfD
 C: Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 C: Keywords: NAD; oxidoreductase
 F: 8-185/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 31.0%; Score 400.5; DB 1; Length 255;
 Best Local Similarity 37.1%; Pred. No. 1.4e-24;
 Matches 96; Conservative 45; Mismatches 107; Indels 11; Gaps 6;

QY 1 MSNRLDGKVAITGGTGLGATATKFFVEGAKVMTDRHSDVGEKAASVGTDPQIQFF 60
 DB 1 MIMNLTDKTVLTGGTGLGATATKFFVEGAKVMTDRHSDVGEKAASVGTDPQIQFF 59

QY 61 QHDSDEDEGWTKLFDATKAFGVPSTLVNAGIAVKNKSVETTTAEWRKLLAVNLGCVFF 120
 DB 60 QTDITDEAACQHAVESAVHTFGDLVNLNAGIEIYIHEMELSDNKNVQLVNLGCVFF 119

QY 121 GTRLGTRQMKNGKLGASIIINSSIEGFGVDPGSLGAYNASKGAVRIMSKSAALCALDKYD 180

Db 120 MSKHALKHLAAGK-G-NIINTSVGLVAMPDIPAYNASKGVLQLTSMAYDYA--KHQ 176
QY 181 VRVTVHPGYIKTLP-----VDLPGA-EEAMSORTK-TPMGHIGEPNDIAICVYLASN 233
Db 177 IRVNCVCPGIIIDTPLNEKSFLENNGTLEIEIKKAKVNPLRLKGPBEIANVMLFLASD 236
QY 234 ESKFATGSEFVVGGYTAQ 252
Db 237 LSSYMTGSAITADGGYTAQ 255
RESULT 5
S48129
3(or 17)beta-hydroxysteroid dehydrogenase (EC 1.1.1.51) - Comamonas testosteroni (ATCC 29412)
C:Species: Comamonas testosteroni
A:Variety: ATCC 11996
C:Date: 14-Jul-1995 #sequence_revision 01-Dec-1995 #text_change 08-Oct-1999
C:Accession: S48129; S51780; S15390; S62216; S62182
R:Abalain, J.H.; di Stefano, S.; Anet, Y.; Quemener, E.; Abalain-Colloc, M.L.; Floch, H.
J. Steroid Biochem. Mol. Biol. 44, 133-139, 1993
A:Title: Cloning, DNA sequencing and expression of (3-17)beta-hydroxysteroid dehydrogenase
A:Reference number: S48129; MUID:93176721
A:Accession: S48129
A:Molecule type: DNA
A:Residues: 1-254 <ABA>
A:Cross-references: EMBL:X63379
A:Note: The source is designated as Pseudomonas testosteroni
R:Abalain, J.H.
submitted to the EMBL Data Library, November 1991
A:Reference number: S51780
A:Accession: S51780
A:Molecule type: DNA
A:Residues: 1-13, 'VV', 16-254 <ABW>
A:Cross-references: EMBL:X63379; NID:9312918; PIDN:CAAA4977.1; PID:g312919
A:Note: The source is designated as Pseudomonas testosteroni
R:Yin, S.J.; Vagelopoulos, N.; Lundquist, G.; Joernvall, H.
Eur. J. Biochem. 197, 359-365, 1991
A:Title: Pseudomonas 3-beta-hydroxysteroid dehydrogenase. Primary structure and relation
A:Reference number: S15390; MUID:91224127
A:Accession: S15390
A:Molecule type: protein
A:Residues: 2-40, 'E', 41-176, 178-240, 'G', 242-254 <YIN>
A:Note: The source is designated as Pseudomonas testosteroni
R:Benach, J.; Knapp, S.; Oppermann, U.C.T.; Haeggglund, O.; Joernvall, H.; Ladenstein, R.
Eur. J. Biochem. 236, 144-148, 1996
A:Title: Crystallization and crystal packing of recombinant 3 (or 17) beta-hydroxysteroid
A:Reference number: S62216; MUID:96184891
A:Accession: S62216
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 2-254 <BEN>
R:Bocco, J.L.; Panzetta, G.; Actis, L.A.; Genti-Raimondi, S.
submitted to the EMBL Data Library, July 1993
A:Description: Nucleotide sequence of the beta-hydroxysteroid dehydrogenase from Pseudom
A:Reference number: S62182
A:Accession: S62182
A:Molecule type: DNA
A:Residues: 1-40, 'E', 41-176, 178-254 <BOC>
A:Cross-references: EMBL:L08971; NID:g309859; PIDN:AAA25742.1; PID:g309860
A:Note: The source is designated as Pseudomonas testosteroni
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C:Keywords: oxidoreductase
F:2-254/product: 3(or 17)beta-hydroxysteroid dehydrogenase #status experimental <MAT>
F:8-185/Domain: short-chain alcohol dehydrogenase homology <SADH>
Query Match 30.5%; Score 393; DB 2; Length 254;
Best Local Similarity 36.7%; Pred. No. 5.4e-24;
Matches 92; Conservative 49; Mismatches 100; Indels 10; Gaps 6;
QY 1 MSNRLDGKVAITGGTIGIGLAIATKFFVEGAKVMITDRHSDVGEKAASVGTPTDQIOFF 60
Db 1 MTRNLQGVALTGTGASGVLEVYKLLIGEGAKVAFSDINA-AGQQLAAELG--ERSNFV 57

QY 61 OHDSDEDEGWTKLDATEKAFGVPSTLVNAGIANKSVSEETTTAEWRKLLAVNLGVFF 120
Db 58 REDVSEADTWLMAVORRLCTLVNAGIILLPGDMETGRLEDFSRLLKINTESVFI 117
QY 121 GYRLGIQRMKNGKLGASIIINSSIEFGVDPGLGAYNASKGAVRIMSKSAALDCAKDYD 180
Db 118 GCQOQIAAMKE--TGSIIINMASVSWLPFIEQYAGYSASKAAVSALTAAALSCRRQGYA 175
QY 181 V-RVNTVHPGYIKTPLYD-DLP---GAERMSQRTKTPMGHIGEPNDIAICVYLASNES 235
Db 176 IRRVNSIHPDGIYTPMQQASLPKGVSKEMVLHDPKLNLRAGRAYMPEIRIAQLVFLASDES 235
QY 236 KEATGSEFVVD 246
Db 236 SVMSGSELHAD 246
RESULT 6
S47055
hypothetical protein 5 - Xanthobacter sp.
C:Species: Xanthobacter sp.
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999
C:Accession: S47055
R:Swaving, J.; Weijers, C.A.G.M.; van Ooyen, A.J.J.; de Bont, J.A.M.
submitted to the EMBL Data Library, June 1994
A:Description: Plenmentation of Xanthobacter Py2 mutants in epoxyalkane degradation; e
A:Reference number: S47051
A:Accession: S47055
A:Molecule type: DNA
A:Residues: 1-249 <SWA>
A:Cross-references: EMBL:X79863; NID:g520947; PIDN:CAA56245.1; PID:g520952
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
F:5-181/Domain: short-chain alcohol dehydrogenase homology <SADH>
Query Match 30.3%; Score 391; DB 2; Length 249;
Best Local Similarity 38.9%; Pred. No. 7.6e-24;
Matches 98; Conservative 39; Mismatches 105; Indels 10; Gaps 6;
QY 5 LDGKVAITGGTIGIGLAIATKFFVEGAKVMITDRHSDVGEKAASVGTPTDQIOFFQHDS 64
Db 2 LDAEVIAITGGAGIGLAVAHAAIRAGARVALIDRDGACQRAAAEFGA--AAWGVGADV 59
QY 65 SDEGWTKLDATEKAFGVPSTLVNAGIANKSVSEETTTAEWRKLLAVNLGVFFGTRL 124
Db 60 TDEAAITAMAGAQALGPLTGLVNNAGIAGVHATEVETWSRIMAVNVVTGTFELASKA 119
QY 125 GIQRMKNGKLGASIIINSSIEFGVDPGLGAYNASKGAVRIMSKSAALDCAKDYDVVN 184
Db 120 ALFGMLERGRGA-IVNFGSVAGLVGIPDMAAYCAKGAVVNLTRQMAADYSGR--GIRVN 176
QY 185 TVHPGYIK-TPLVDDLPAGE---EAMSOR-TKTPMGHIGEPNDIAICVYLASNESKFAT 239
Db 177 VVCPGTAVAGTDMGROLLGTDGPELEARRLAKYPMGRFGTPEIDIAEAAVFLSLTKAAFTV 236
QY 240 GSEFVVDGSGYTA 251
Db 237 GSVLAVDGGMTA 248
RESULT 7
E72427
oxidoreductase, short chain dehydrogenase/reductase family - Thermotoga maritima (str
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: E72427
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A:Reference number: A72200; MUID:99287316
A:Accession: E72427

C:Accession: B95284
R:Barrett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti*
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: B95284
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-253 <KUR>
A:Cross-references: GB:AE006469; PIDN:AAK64836.1; PID:g14523249; GSPDB:GN00165
A:Experimental source: Strain 1021, megaplasmid pSymA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Wiedner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Sma0329
A:Genome: plasmid
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 28.9%; Score 372.5; DB 2: Length 253;
Best Local Similarity 37.7%; Pred. No. 2.3e-22;
Matches 97; Conservative 46; Mismatches 93; Indels 21; Gaps 8;
QY 1 MSNRLDGKVAITGTGIGLAIAATKFEVEGAKVMITDRH-----SDVGEKAASVGTDPQ 56
DB 1 MSKRPDGRVAITVGGSGGIAAIAANRLLEEGASVMSGRTERKRLSDVASKM-----PADR 55
QY 57 IQPFOHDSDEGWTGKLFDATEKAFGVPVSTLVNAGIANKSVETTTAEWRKLLAVNL 116
DB 56 SGIFVANVSSRRPDCDALVAATVERGRDITVVNAGMNFVGTIOETSDQWDECIAASDL 115
QY 117 GVFFGTRIGLQIRMK-NKGLGASIIINMSIEGVPDPSLGAYNASKGAVRINSKSAALDCA 175
DB 116 GVFFMSRAAHPILKETG---SIVNIGSVSSLGGSWHAAYNAAGGVANLTRSAA--CD 170
QY 176 LKDYDVRVNTVHPGYIKTPLVDLPGAEAMSQRT--KTPMGHIGEPNDIAYICVYLASN 233
DB 171 LKGFVRANTVAPGLTVTGVMVEAIND--DDALLEKAWDRIPRRAGQ---ASAVAFASD 226
QY 234 ESKFATGSEFFVDDGGYT 250
DB 227 EAAWITGIVLPVDDGGT 243

RESULT 11
JS0385
glucose 1-dehydrogenase (EC 1.1.1.47) - *Bacillus megaterium*
C:Species: *Bacillus megaterium*
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jun-1999
C:Accession: J39852; JS0385
R:McCamra, T.; Eboro, R.V.; Nakai, T.; Makino, Y.; Negoro, S.; Urabe, I.; Okada, H.
J. Ferment. Bioeng. 70, 363-369, 1990
A:Title: Structure of isozyme genes of glucose dehydrogenase from *Bacillus megaterium* IA
A:Reference number: J39850
A:Accession: J39852
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-261 <RES>
A:Cross-references: GB:D90043; NID:g216265; PIDN:BAAL4099.1; PID:g216268
A:Experimental source: strain IAM1030
C:Complex: homotetramer
C:Function:
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C:Keywords: oxidoreductase
F:8-189/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 28.8%; Score 371.5; DB 2: Length 261;
Best Local Similarity 34.2%; Pred. No. 2.9e-22;
Matches 88; Conservative 51; Mismatches 105; Indels 13; Gaps 5;
QY 1 MSNRLDGKVAITGTGIGLAIAATKFEVEGAKVMITDRHSDVGEKA-----AKSVGTP 54
DB 1 MYKDLEGKVVITGSGTGLGKAMAFRFAEKAKVAVVYRSKE--EANSVLEEEKVGV-- 56
QY 55 DOIQFOHDSDEGWTGKLFDATEKAFGVPVSTLVNAGIANKSVETTTAEWRKLLAVNL 114
DB 57 GEAIKAVKGVDTTVESDVINIVQSSIKREFGKLDVINNAGMENPVSSHEMSLSDWKNKVIDTN 116
QY 115 LDGVFFGTRIGLQIRMK-NKGLGASIIINMSIEGVPDPSLGAYNASKGAVRINSKSAALDCA 174
DB 117 LGAFGLSREAIKYFVENDIKGTVINNMSVHEKIPWPLFVHTAASKGMKMTETLALEY 176
QY 175 ALKDYDVRVNTVHPGYIKTPL-VDDLPGAEAMSQRTKTPMGHIGEPNDIAYICVYLASN 233
DB 177 APK--GIRVNNIGPGAINTPINAEKFADEQRADEVSMIPMGVIGEPPEEIAAVALASS 234
QY 234 ESKFATGSEFFVDDGGYT 250
DB 235 EASYVTGITLFDAGGMT 251

RESULT 12
A33528
glucose 1-dehydrogenase (EC 1.1.1.47) - *Bacillus megaterium*
C:Species: *Bacillus megaterium*
C>Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 11-Jun-1999
C:Accession: A33528
R:Makino, Y.; Negoro, S.; Urabe, I.; Okada, H.
J. Biol. Chem. 264, 6381-6385, 1989
A:Title: Stability-increasing mutants of glucose dehydrogenase from *Bacillus megateri*
A:Reference number: A33528; MUID:89197943
A:Accession: A33528
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-261 <MAK>
A:Cross-references: GB:J04805; NID:g142974; PIDN:AAA22475.1; PID:g142975
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C:Keywords: oxidoreductase
F:8-189/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 28.7%; Score 370.5; DB 2: Length 261;
Best Local Similarity 33.6%; Pred. No. 3.5e-22;
Matches 86; Conservative 51; Mismatches 108; Indels 11; Gaps 4;
QY 1 MSNRLDGKVAITGTGIGLAIAATKFEVEGAKVMIT-----DRHSDVGEKAASVGTDP 55
DB 1 MYKDLEGKVVITGSGTGLGKSMARFARFAEKAKVAVVYRSKEDEANSVLEEEKVGEAI 60
QY 56 IQQFOHDSDEGWTGKLFDATEKAFGVPVSTLVNAGIANKSVETTTAEWRKLLAVNL 115
DB 61 AV---KGVDTTVESDVINLVQSAIKREFGKLDVINNAGLENPVSSHEMSLSDWKNKVIDTNL 117
QY 116 DGVFFGTRIGLQIRMK-NKGLGASIIINMSIEGVPDPSLGAYNASKGAVRINSKSAALDCA 175
DB 118 TGAFLGSRKAIKYFVENDIKGTVINNMSVHEKIPWPLFVHTAASKGMKMTETLALEYA 177
QY 176 LKDYDVRVNTVHPGYIKTPL-VDDLPGAEAMSQRTKTPMGHIGEPNDIAYICVYLASNE 234
DB 178 PK--GIRVNNIGPGAINTPINAEKFADEQRADEVSMIPMGVIGEPPEEIAAVALASS 235
QY 235 SKFATGSEFFVDDGGYT 250
DB 236 ASYVTGITLFDAGGMT 251

RESULT 13
B86737
acetoin dehydrogenase (EC 1.1.1.5) [Imported] - *Lactococcus lactis* subsp. *lactis* (str

N:Alternate names: acetoin reductase
 C:Species: Lactococcus lactis subsp. lactis
 C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
 C:Accession: B86737
 R:Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich Genome Res. 11, 731-753, 2001
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. Genome Res. 11, 731-753, 2001
 A:Reference number: A86625; MUID:2125186; PMID:11337471
 A:Accession: B86737
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-253 <STO>
 A:Cross-references: GB:AE005176; PID:g12723829; PIDN:AAK04996.1; GSPDB:GN00146
 A:Experimental source: strain IL1403
 C:Genetics:
 A:Gene: butA
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 C:Keywords: oxidoreductase

Query Match 28.5%; Score 368; DB 2; Length 253;
 Best Local Similarity 34.3%; Pred. No. 5.3e-22;
 Matches 86; Conservative 48; Mismatches 103; Indels 14; Gaps 4;

QY 8 KVALITGGTIGLAIATKFEVCAKVMITDRHSDVCEKAASVGTDPQIQFQHDSSDE 67
 DB 3 KIAVVGAGGIGFALAKRLYNDGFRVITDIYNEETAQAKAEIG--ENSFAIKADYSDR 60

QY 68 DGTWTKLFDATKAFPGVSTLVNAGIAVNSVEETTTAEWRKLLAVNLDGVFEFTRLGIQ 127
 DB 61 EQVISALNAVVDGDLNVVNNAGIAPTQIETIPEQPHQYNNVNGVGLNGTQNSTA 120

QY 128 RMKNGKLGASIIINMSIEGFGVPSGLAYNASKGAVRMSKAALDCAKDYDVRVTNH 187
 DB 121 LFRKLGHGKIIINATSOAGVYVGNPNLMYSSKFAVRGMTQIAARD--LAEEGITVNAVYA 178

QY 188 PGVIKTPLVDDL-----PGAEMSQR--KTPMGHIGEPNDIAYICVYLASNEKF 237
 DB 179 PGIVKTPMFEDIAHGVKNAGKDEMGMTQFAKDIAKRLSEPEDVANVVSFLAGPDSNY 238

QY 238 ATGSEFVDDG 248
 DB 239 ITGQTIIVDGG 249

RESULT 14
 C0885
 probable dehydrogenase - Mycobacterium tuberculosis (strain H37Rv)
 C:Species: Mycobacterium tuberculosis
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
 C:Accession: C70885
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987
 A:Accession: C70885
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-258 <COL>
 A:Cross-references: GB:AL008883; GB:AL123456; NID:g3261490; PIDN:CAA15519.1; PID:g3261280
 A:Experimental source: strain H37Rv
 C:Genetics:
 A:Gene: Rv2857c
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 F:11-188/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 28.4%; Score 367; DB 2; Length 258;
 Best Local Similarity 35.7%; Pred. No. 6.5e-22;
 Matches 92; Conservative 45; Mismatches 105; Indels 16; Gaps 7;

QY 1 MSNRDGLKVAITGTLGIGLAIATKFEVCAKVMITDRHSDVGEKAASVGTDPQIQ-- 58

Db 4 LSQRLAGRAVITGGSGIGLAAGRRMRAEGATIVGVDVVEAGGAA-----DELSGL 57
 QY 59 FFOHDSDEGWTYKLFDATEKAFPGVSTLVNAGIA--VNKSVEETTTAEWRKLLAVNLD 116
 Db 58 FVPTDVCDEDAVNGFLFGAAETGRIDIAFNAGISPPEDNLIENATLAARQVQDVNLK 117
 QY 117 GVFEGRTRGTRQMKNGKLGASIIINMSIEGFGV--PSLGAYNASKGAVRMSKAALDCA 175
 Db 118 SVLYCCRAALRHVVLAKG--SIVNTASFVAVGATSQISTASKGGVLAWSRELGVQVFA 176
 QY 176 LKDYDVRVNTVHPGYIKTPLVDDL--PGAEMSQRKTPMGHIGEPNDIAYICVYLASN 233
 Db 177 RQ--GIRVNALCPGVNTPLQLQELFAXNPERAARMVHVPLGRFAEPDEIAAAVFLASD 234
 QY 234 ESKFATGSEFVDDGYTA 251
 Db 235 DASFITASTFLVDGGISS 252

RESULT 15

A99950

hypothetical protein SA2260 [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C:Accession: A99950

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cut, L.;

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, R.; Inoue, R.; Kaito, C.; Sekimizu,

C.; Shiba, T.; Hatcori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: A99950

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-272 <KUR>

A:Cross-references: GB:BA000018; PID:g13702422; PIDN:BABA3563.1; GSPDB:GN00149

A:Experimental source: strain N315

C:Genetics:

A:Gene: SA2260

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 28.4%; Score 366; DB 2; Length 272;

Best Local Similarity 35.4%; Pred. No. 8.4e-22;

Matches 91; Conservative 44; Mismatches 108; Indels 14; Gaps 6;

QY 4 RLDGKVAITGTLGIGLAIATKFEVCAKVMITDRHSDVGEKAASVGTDPQIQFQHD 63

Db 3 RLENKVAVVTGASTGIGQASAIALAQEGAYVLAVDAEAVSETVVDKTKSNGDNAKAYNVD 62

QY 64 SDEDGWTCLFDATKAFGVPSTLVNAGI--AVNKSVEETTTAEWRKLLAVNLDGVFFG 121

Db 63 ISDEQVDFVSDIKQFGRIDVLFNNAGVDNAAGR--IHEYIPIDVDYDKIMNVDMRGFTLM 121

QY 122 TRLGIRMQMKNGKLGASIIINMSIEGFGVDP--PSLGAYNASKGAVRMSKAALDCAKDYD 181

Db 122 TKMMLPLMNQ--GGSIVNTSFGQADLYRSGYNAAGAVINFTKSIAYEVG-RD-GI 177

QY 182 RVNTVHPGYIKTPLVDDLPGAEE-----AMSORTKTPMGHIGEPNDIAYICVYLASN 234

Db 178 RSNAIAPGTIETPLVDKLTGTSDDAGKTFREKQKWTPLGLRGKPEVAKLVVFLASDD 237

QY 235 SKFATGSEFVDDGYTA 251

Db 238 SSFITGETTRIDGVNMA 254

Search completed: October 30, 2002, 15:46:26

Job time : 22 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 30, 2002, 15:45:05 ; Search time 12 Seconds
(without alignments)

813.111 Million cell updates/sec

Title: US-09-910-033A-2

Perfect score: 1290

Sequence: 1 MSNRLDGKVAITGTLGIG.....NESKATGSEFVVDGGYTAQ 252

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	464.5	36.0	260	1 YK02_MYCTU	Q10855 mycobacteri
2	441.5	34.2	250	1 LINC_PSEPA	P50198 pseudomonas
3	407.5	31.6	255	1 2BHD_STREX	P19992 streptomyce
4	400.5	31.0	255	1 YWFD_BACSU	P39640 bacillus su
5	383	29.7	256	1 Y019_THEMA	Q56318 thermotoga
6	380	29.5	247	1 YD50_MYCTU	Q11020 mycobacteri
7	371.5	28.8	261	1 DHG1_BACME	P39482 bacillus me
8	370.5	28.7	261	1 DHG2_BACME	P40288 bacillus me
9	370	28.7	253	1 3BHD_COMTE	P19871 comamonas t
10	365.5	28.3	246	1 FBAG_THEMA	Q9x248 thermotoga
11	363.5	28.2	261	1 DHGA_BACME	P10528 bacillus me
12	360	27.9	262	1 DHGB_BACME	P07999 bacillus me
13	358.5	27.8	261	1 DHG_BACSU	P12310 bacillus su
14	357.5	27.7	261	1 DHG4_BACME	P39485 bacillus me
15	355.5	27.6	261	1 DHG2_BACME	P39483 bacillus me
16	352.5	27.3	261	1 DHG3_BACME	P39484 bacillus me
17	351.5	27.2	251	1 Y325_THEMA	Q9wyq0 thermotoga
18	348.5	27.0	258	1 DHG2_BACSU	P80869 bacillus su
19	345	26.7	261	1 DHB8_HUMAN	Q92506 homo sapien
20	339.5	26.3	256	1 BUDC_KLEPN	Q84336 klebsiella
21	326	25.3	285	1 G539_BACSU	P80873 bacillus su
22	325.5	25.2	260	1 DHB8_MOUSE	P50171 mus musculu
23	324	25.1	336	1 TS2_WAIZE	P50160 zea mays (m
24	322	25.0	289	1 YHDE_BACSU	Q07575 bacillus su
25	321	24.9	248	1 FBAG_CHLMU	Q9pkf7 chlamydia m
26	321	24.9	548	1 YAVI_RHISN	Q53217 rhizobium s
27	319.5	24.8	256	1 GNO_GLUOX	P50199 gluconobact
28	319.5	24.8	258	1 BDBA_RHIME	Q86034 rhizobium m
29	318	24.7	244	1 FBAG_VIBCH	Q9kqh7 vibrio chol
30	317.5	24.6	262	1 VERL_ASPPA	P50161 aspergillus
31	317	24.6	241	1 PHBB_ZOORA	P32338 zoogloea ra
32	316	24.5	246	1 FBAG_BACSU	P51831 bacillus su
33	316	24.5	281	1 SOUL_CANAL	P87219 candida alb

34	313.5	24.3	264	1 STCU_EMENI	Q00791 emericeila
35	312	24.2	241	1 PHBB_RHIME	P50205 rhizobium m
36	312	24.2	248	1 FBAG_AQUAE	O67610 aquifex aeo
37	310.5	24.1	271	1 SDRL_PICAB	Q08632 picea abies
38	310	24.0	273	1 TRNL_DATST	P50162 datura stra
39	307.5	23.8	250	1 LINC_PSEPA	P50197 pseudomonas
40	305	23.6	247	1 FBAG_CHLTR	P38004 chlamydia t
41	305	23.6	285	1 YHXC_BACSU	P40397 bacillus su
42	304.5	23.6	248	1 FBAG_CHLPN	Q9z8p2 chlamydia p
43	303	23.5	278	1 YALA_RHISN	P55541 rhizobium s
44	301.5	23.4	320	1 FBAG_CUPLA	P28643 cuphea lanc
45	299.5	23.2	253	1 Y4MP_RHISN	P55575 rhizobium s

ALIGNMENTS

RESULT 1					
YK02_MYCTU					
ID	YK02_MYCTU	STANDARD;	PRT;	260 AA.	
AC	Q10855;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	15-JUL-1999 (Rel. 38, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Putative oxidoreductase RV2002 (EC 1.-.-.-)				
GN	FBAG3 OR RV2002 OR MT2058 OR MTCY39.16C.				
OS	Mycobacterium tuberculosis.				
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;				
OC	Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.				
OX	NCBI_TaxID=1773;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=H37RV;				
EX	MEDLINE=98295987; PubMed=9634230;				
RA	Coile S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,				
RA	Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,				
RA	Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,				
RA	Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,				
RA	Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,				
RA	Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,				
RA	Rutter S., Seeger K., Skelton S., Squares S., Squares R.,				
RA	Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;				
RT	*Deciphering the biology of Mycobacterium tuberculosis from the				
RT	complete genome sequence.*;				
RL	Nature 393:537-544(1998).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CDC 1551 / Oshkosh;				
RA	Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,				
RA	Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,				
RA	Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,				
RA	Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,				
RA	Bisbal W.;				
RT	*Whole genome comparison of Mycobacterium tuberculosis clinical and				
RT	laboratory strains.*;				
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.				
CC	-1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES				
CC	(SDR) FAMILY.				

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EMBL; Z44025; CAA98414.1; --
EMBL; AE007057; AAK46335.1; --
HSSP; P19992; 1HDC.
TIGR; MT2058; --
Tuberculist; RV2002; --
InterPro; IPR002198; ADH_short.

```

DR PFam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
FT NP_BIND 11 35 NAD (BY SIMILARITY).
FT ACT_SITE 153 153 BY SIMILARITY.
FT CONFLICT 174 174 S -> G (IN REF. 2).
SQ SEQUENCE 260 AA; 27030 MW; 0935A14ED36220B7 CRC64;

Query Match 36.0%; Score 464.5; DB 1; Length 260;
Best Local Similarity 42.2%; Pred. No. 6.6e-31;
Matches 106; Conservative 44; Mismatches 90; Indels 11; Caps 5;

QY 1 MSNRLDGKVAIIIGTIGIGLATATKFEVGEKAKVMTDRSDVGEKAKSVGTPDQIQFF 60
DB 1 MSGRLGKVALVSGGAGMASHVRAMVGEKAKVFGDILDEEKAVAAELA--DAARYV 58
QY 61 QHSDSDGWTKLFDATKAFGPVSTLVNNAAGIANKSVETTTAEWRKLLAVNL 120
DB 59 HLDVTPQAQTAADVAVTAFGLHLVNNAGILNIGTIEDYALTEQRILDVNLTVGL 118
QY 121 GTRIGTORMKNGKLGASIIINSSIEGLAGTVAGCHGTATKFAVRGLTKSTALE--LPSG 175
DB 119 GIRAVKPKMEAGRG--SIINSSIEGLAGTVAGCHGTATKFAVRGLTKSTALE--LPSG 175
QY 181 VRVTVHPGIKPLVDLPCAEAMSQRTKTPMGHIGEPNDIAYICVYLASNEKSFATG 240
DB 176 IRVNSIHGVLKTPMTDWP--EDIF---QTALGRAAEPEVSNLVYLASDESSYSTG 229
QY 241 SEFVVDGGTVA 251
DB 230 AEFVVDGGTVA 240

RESULT 2
LINK_PSEPA
ID LINK_PSEPA STANDARD; PRT; 250 AA.
AC P50198;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (EC 1.1.1.-.-)
GN LINK.
OS Pseudomonas paucimobillis (Sphingomonas paucimobillis).
OC Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
OC Sphingomonas.
OX NCBI_TaxID=13689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UT26;
RX MEDLINE=94252977; PubMed=7515041;
RA Nagata Y., Ohtomo R., Miyauchi K., Fukuda M., Yano K., Takagi M.;
RT "Cloning and sequencing of a 2,5-dichloro-2,5-cyclohexadiene-1,4-diol
RT dehydrogenase gene involved in the degradation of gamma-
RT hexachlorocyclohexane in Pseudomonas paucimobillis.";
RL J. Bacteriol. 176:3117-3125(1994).
CC -!- FUNCTION: DEGRADATION OF 2,5-DICHLORO-2,5-CYCLOHEXADIENE-1,4-DIOL
CC (2,5-DDOL) INTO 2,5-DICHLOROHYDROQUINONE (2,5-DCHO). LINK IS NOT
CC ESSENTIAL TO GAMMA-HCH DEGRADATION.
CC -!- PATHWAY: DEGRADATION OF GAMMA-HEXACHLOROCYCLOHEXANE.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC -----
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CC or send an email to a license@isb-sib.ch).
CC -----
CC EMBL; D23722; BAA04939.1; -

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DR HSP: P19992; LHDC.
DR InterPro: IPR002198; ADH_short.
DR PFam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.
FT NP_BIND 9 34 NAD (BY SIMILARITY).
FT ACT_SITE 156 156 BY SIMILARITY.
SQ SEQUENCE 250 AA; 25492 MW; 8C52703FF76382CF CRC64;

Query Match 34.2%; Score 441.5; DB 1; Length 250;
Best Local Similarity 41.0%; Pred. No. 4.7e-29;
Matches 105; Conservative 43; Mismatches 93; Indels 15; Gaps 6;

QY 1 MSNRLDGKVAIIIGTIGIGLATATKFEVGEKAKVMTDRSDVGEKAKSV-----GTPD 55
DB 1 MANRLAGKVALITGGASGLGAQAQKRAEAGKVI---GDLNEEMAKGVAAEIRAAG 56
QY 56 QIOFFHSDSDGWTKLFDATKAFGPVSTLVNNAAGIANKSVETTTAEWRKLLAVNL 115
DB 57 DALFRLDVTDAASNNNAIAAAYDVGGLTTLNTAGLIHPGGFEESIEGWNKMWAVNQ 116
QY 116 DGVFFGTRIGIORMKNGKLGASIIINSSIEGLAGTVAGCHGTATKFAVRGLTKSTALE--LPSG 175
DB 117 TAIFLAGTKAAIPELVKSGNG--SIINSSIEGLAGTVAGCHGTATKFAVRGLTKSTALE--LPSG 175
QY 176 LKDYDVRYVTVHPGIKPLVDLPCAEAMSQRTKTPMGHIGEPNDIAYICVYLASNE 234
DB 174 FVDRGVRYVTVHPGMNTPITANVP--PDVLKQOTSQIPMGKLGDPIDIANGLFLASDE 231
QY 235 SKFATGSEFVVDGGYT 250
DB 232 AKYITGVLDLPIDGWS 247

RESULT 3
2BHD_STREX
ID 2BHD_STREX STANDARD; PRT; 255 AA.
AC P19992;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE 20-beta-hydroxysteroid dehydrogenase (EC 1.1.1.53).
OS Streptomyces exfoliatus (Streptomyces hydroganens).
OC Bacteria; Firmicutes; Actinobacteria; Actinomycetaceae;
OC Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1905;
RN [1]
RP SEQUENCE.
RX MEDLINE=90306362; PubMed=2194840;
RA Marekov L., Krook M., Joernvall H.;
RT "Prokaryotic 20 beta-hydroxysteroid dehydrogenase is an enzyme of the
RT short-chain, non-metalloenzyme' alcohol dehydrogenase type.";
RL FEBS Lett. 266:51-54(1990).
RN [2]
RX X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RP MEDLINE=92052211; PubMed=1946424;
RA Ghosh D., Weeks C.M., Grochulski P., Duax W.L., Erman M.,
RA Rimsay R.L., Orr J.C.;
RT "Three-dimensional structure of holo 3 alpha,20 beta-hydroxysteroid
RT dehydrogenase: a member of a short-chain dehydrogenase family.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:10064-10068(1991).
CC -!- CATALYTIC ACTIVITY: Androstan-3-alpha,17-beta-diol + NAD(+) -> 17-
CC beta-hydroxyandrostan-3-one + NADH.
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR PIR: S10707; S10707.
DR PDB: 2HSD; 31-AUG-94.
DR PDB: LHDC; 07-FEB-95.
DR InterPro: IPR002198; ADH_short.
DR PFam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.

```

[illegible]


```

RN  SEQUENCE FROM N.A.
RP  STRAIN-1AM 1030;
RC  Mitamura T., Ebara R.V., Nakai T., Makino Y., Negoro S., Urabe I.,
RA  Okada H.;
RT  "Structure of isozyme genes of glucose dehydrogenase from Bacillus
RL  megaterium IAM1030."
RJ  J. Ferment. Bioeng. 70:363-369(1990).
CC  -!- FUNCTION: MAY PLAY SOME ROLE IN SPORE GERMINATION.
CC  -!- CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+) = D-glucono-1,5-
CC  lactone + NAD(P)H.
CC  -!- SUBUNIT: HOMOTETRAMER.
CC  -!- DEVELOPMENTAL STAGE: EXPRESSED DURING SPORULATION.
CC  -!- MISCELLANEOUS: PREFERS NADP TO NAD.
CC  -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC  (SDR) FAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; D90043; BAAL4099.1; -.
DR  PIR; JS0385; JS0385.
DR  HSSP; P50163; 2AE1.
DR  InterPro; IPR002198; ADH_short.
DR  Pfam; PF00106; adh_short; 1.
DR  PRINTS; PR00080; SDRFAMILY.
DR  PROSITE; PS00061; ADH_SHORT; 1.
KW  Oxidoreductase; NADP; Multigene family; Sporulation; Germination.
FT  NP_BIND 11 35 NADP (BY SIMILARITY).
FT  ACT_SITE 158 158 BY SIMILARITY.
FT  SEQUENCE 261 AA; 28117 MW; B92B72889A160335 CRC64;

Query Match      28.8%; Score 371.5; DB 1; Length 261;
Best Local Similarity 34.2%; Pred. No. 2.5e-23;
Matches 88; Conservative 51; Mismatches 105; Indels 13; Gaps 5;

QY  1 MSNRLDGKVAITGGTGLGIGLAIAATKFEVGEAKVMTDRHSDVGEKA-----AKSVGTP 54
DB  1 MYKDLGKVVVITGSTGLGSKMAIFPATEKAKVVVYNSKKE--EANSVLVEIKKVG-- 56

QY  55 DQIQFQHDSDDEGWTGLFDATEAFGPVSTLVNAGIAVNKSVETTTAEWRKLLAVN 114
DB  57 GEALAVKGDVTVESDVINLVQSSIKFEGKLDVMINNAGHENPVSSHMSLSDNKVIDTN 116

QY  115 LDGVFFGTRGLGIQRMKNKGLGASIIINMSSIEGFVGDPSLGAYNASKGAVRIMSKSAALDC 174
DB  117 LGAFGLGSRGAIKYFVENDIKGTVINMSSVHEKIPWPLFVHYAASKGKMLMTETLLEY 176

QY  175 ALKDYDVRYNTVHPGYIKTPL-VDDLPGAEEAMSORTKTPMGHIGEPNDIAYICVILASN 233
DB  177 APK--GIRVNNIGPGAINTPINAEKPADPQADVESMIPMGYIGEPEEIAAVALASS 234

QY  234 ESKFATGSEFVVDGGYT 250
DB  235 EASYVTGITLFDAGGMT 251

RESULT 8
DHG_BACME STANDARD; PRT; 261 AA.
AC  P40288.
DT  01-FEB-1995 (Rel. 31, Created)
DT  01-FEB-1995 (Rel. 31, Last sequence update)
DT  01-OCT-1996 (Rel. 34, Last annotation update)
DE  Glucose 1-dehydrogenase (EC 1.1.1.47).
OS  Bacillus megaterium.
OC  Bacteria; Firmicutes; Bacillus/Clostridium group;
OC  Bacillus/Staphylococcus group; Bacillus.
OX  NCBI_TaxID=1404;

```

```

RN  SEQUENCE FROM N.A., SEQUENCE OF 1-29, AND MUTAGENESIS.
RP  STRAIN-IMG3;
RC  MEDLINE-89197943; PubMed-2495285;
RA  Makino Y., Negoro S., Urabe I., Okada H.;
RT  "Stability-increasing mutants of glucose dehydrogenase from Bacillus
RL  megaterium IMG3."
RJ  J. Biol. Chem. 264:6381-6385(1989).
CC  [2]
CC  REVISIONS.
CC  Urabe I.;
CC  Submitted (MAR-1989) to the EMBL/GenBank/DBJ databases.
CC  -!- CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+) = D-glucono-1,5-
CC  lactone + NAD(P)H.
CC  -!- SUBUNIT: HOMOTETRAMER.
CC  -!- DEVELOPMENTAL STAGE: EXPRESSED DURING SPORULATION.
CC  -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC  (SDR) FAMILY.
CC  -----
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; J04805; AAA22475.1; -.
DR  PIR; A33528; A33528.
DR  HSSP; P50163; 2AE1.
DR  InterPro; IPR002198; ADH_short.
DR  Pfam; PF00106; adh_short; 1.
DR  PRINTS; PR00080; SDRFAMILY.
DR  PROSITE; PS00061; ADH_SHORT; 1.
KW  Oxidoreductase; NADP; Multigene family; Sporulation.
FT  NP_BIND 11 35 NADP (BY SIMILARITY).
FT  ACT_SITE 158 158 BY SIMILARITY.
FT  MUTAGEN 96 96 E->A,G,K; HEAT STABLE.
FT  MUTAGEN 108 108 D->N; HEAT STABLE.
FT  MUTAGEN 112 112 V->A; HEAT STABLE.
FT  MUTAGEN 133 133 E->K; HEAT STABLE.
FT  MUTAGEN 183 183 V->I; HEAT STABLE.
FT  MUTAGEN 194 194 P->Q; HEAT STABLE.
FT  MUTAGEN 210 210 E->K; HEAT STABLE.
FT  MUTAGEN 217 217 Y->H; HEAT STABLE.
FT  MUTAGEN 252 252 Q->L; HEAT STABLE.
FT  MUTAGEN 253 253 Y->C; HEAT STABLE.
FT  MUTAGEN 258 258 A->G; HEAT STABLE.
SQ  SEQUENCE 261 AA; 28085 MW; C23AC98D304EEB2F CRC64;

Query Match      28.7%; Score 370.5; DB 1; Length 261;
Best Local Similarity 33.6%; Pred. No. 3e-23;
Matches 86; Conservative 51; Mismatches 108; Indels 11; Gaps 4;

QY  1 MSNRLDGKVAITGGTGLGIGLAIAATKFEVGEAKVMT-----DRHSDVGEKAASVGTDP 55
DB  1 MYKDLGKVVVITGSTGLGSKMAIFPATEKAKVVVYNSKKEDEANSVLVEIKKVGGEAI 60

QY  56 QIQFQHDSDDEGWTGLFDATEAFGPVSTLVNAGIAVNKSVETTTAEWRKLLAVN 115
DB  61 AV---KGDVTVESDVINLVQSAIKFEGKLDVMINNAGLENPVSSHMSLSDNKVIDTN 117

QY  116 DGVFEFTRGLGIQRMKNKGLGASIIINMSSIEGFVGDPSLGAYNASKGAVRIMSKSAALDC 175
DB  118 TGAFGLGSRGAIKYFVENDIKGTVINMSSVHEKIPWPLFVHYAASKGKMLMTETLLEYA 177

QY  176 LKDYDVRYNTVHPGYIKTPL-VDDLPGAEEAMSORTKTPMGHIGEPNDIAYICVILASN 234
DB  178 PK--GIRVNNIGPGAINTPINAEKPADPQADVESMIPMGYIGEPEEIAAVALASS 235

QY  235 SKFATGSEFVVDGGYT 250
DB  236 ASYVTGITLFDAGGMT 251

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FT ACT_SITE 154 154 BY SIMILARITY.
SQ SEQUENCE 246 AA; 26401 MW; 8C08904D28099142 CRC64;
Query Match 28.3%; Score 365.5; DB 1; Length 246;
Best Local Similarity 35.1%; Pred. No. 7.1e-23;
Matches 87; Conservative 52; Mismatches 100; Indels 9; Gaps 5;
QY 4 RLDGKVAITGGTIGLIGLATKFEVGAQVITDRSDVGEKAASV-GTPDQIOFPQH 62
DB 2 RLEGVCLITGAASGIGKATLLFAOEGATVIAGDISKENLDSLVKEAEGLPGRVDPVL 61
QY 63 DSDDEGWTLEFATEKAFGVPSTLVNNAIVNKSVEETTTAEWRKLLAVNLDCVFFGT 122
DB 62 NVTDROIKEVEKVKQIGRIDVLVNNAGITRDALLVRKMEEDWDVAVINLKGVENVT 121
QY 123 RLQRTKRNKGLGASIIINSSIEGFVGDPSLGAYNASKGAVRIMSKAALDCAKLDVDR 182
DB 122 QMVPYNIKQKNG-SIVNVSVVGIYNGPGTNYAASKAGVIGTKTWAKELAGR--NIR 178
QY 183 VNVVHPCYIKTPLVDDLP--GAEEAMSORTKTPMGHIGEPNDIAYICVYLASNESKFPATG 240
DB 179 VNAVAPGFIETPMTKLPKARETALS---RIPLRGFKPEEVAQVILFLASDESSESVYTG 235
QY 241 SEFVDDGG 248
DB 236 QVIGIDGG 243
RESULT 11
DHGA_BACME STANDARD; PRT; 261 AA.
ID DHGA_BACME
AC F10528;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Glucose 1-dehydrogenase A (EC 1.1.1.47).
GN GDHA.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-M1286;
RX MEDLINE=88271315; PubMed=3134196;
RA Heilmann H.J., Maegert H.J., Gassen H.G.;
RT "Identification and Isolation of Glucose dehydrogenase genes of
RT Bacillus megaterium M1286 and their expression in Escherichia coll.,"
RL Eur. J. Biochem. 174:485-490(1988).
CC -l- CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+) -> D-glucono-1,5-
CC lactone + NAD(P)H.
CC -l- SUBUNIT: HOMOTETRAMER.
CC -l- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X12370; CAA30931.1; -
CC PIR: S00812; S00812.
CC HSSP: P50162; LAEL.
CC InterPro: IPR002198; ADH_short.
CC Pfam: PF00106; adh_short; 1.
CC PRINTS: PR00080; SDRFAMILY.
CC PROSITE: PS00061; ADH_SHORT; 1.
CC Oxidoreductase; NADP; Multigene family.
CC NP_BIND 11 35 NADP (BY SIMILARITY).
CC ACT_SITE 158 158 BY SIMILARITY.
FT

SQ SEQUENCE 261 AA; 28187 MW; 6FADDA3968DC417C CRC64;
Query Match 28.3%; Score 363.5; DB 1; Length 261;
Best Local Similarity 31.5%; Pred. No. 1.1e-22;
Matches 82; Conservative 51; Mismatches 108; Indels 19; Gaps 4;
QY 1 MSNRLDGKVAITGGTIGLIGLATKFEVGAQVITDRSDVGEKAASV 51
DB 1 MYTDLKDKVVVITGGTIGLGRAMAVRFQGEAKVVIYNNNEEALDAKKEVEAGGOAI 60
QY 52 GTPDQIOFPQHSDSDGWTLEFATEKAFGVPSTLVNNAIVNKSVEETTTAEWRKLL 111
DB 61 -----IVOGDVTKEEDVVNLVQTAIKEFTGLDVMNNAGVENPVPSHSLSDLNWVKVI 113
QY 112 AVNLGVFFETRLGIORMKNGKGLGASIIINSSIEGFVGDPSLGAYNASKGAVRIMSKAA 171
DB 114 DTNLTGAFSLGREAKIKFVENDIKGNVINSSVHEMIPWPLFVHYASKGGMKLTETLA 173
QY 172 LOCALKDYVRVNTVHPGYIKTPL-VDDLFGAEEAMSORTKTPMGHIGEPNDIAYICVYL 230
DB 174 LEVAPK--GIRVNNIGPGAMNTPINAKEKFDADPEQRAVESIMPGYIGKPEEVAVA AFL 231
QY 231 ASNESKFPATGSEFVDDGGYT 250
DB 232 ASSQASYVTGTTLTFADGGMT 251
RESULT 12
DHGB_BACME STANDARD; PRT; 262 AA.
ID DHGB_BACME
AC P07999;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Glucose 1-dehydrogenase B (EC 1.1.1.47).
GN GDHB.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE.
RX MEDLINE=84108870; PubMed=6420184;
RA Jany K.-D., Ulmer W., Froschle M., Pfeleiderer G.;
RT "Complete amino acid sequence of glucose dehydrogenase from Bacillus
RT megaterium,"
RL FEBS Lett. 165:6-10(1984).
RN [2]
RP REVISIONS TO 207 AND 258.
RX MEDLINE=88271315; PubMed=3134196;
RA Jany K.-D.;
RL Unpublished results, cited by:
RL Heilmann H.J., Maegert H.J., Gassen H.G.;
RL Eur. J. Biochem. 174:485-490(1988).
RN [3]
RP SEQUENCE OF 1-52 FROM N.A.
RC STRAIN-M1286;
RX MEDLINE=88271315; PubMed=3134196;
RA Heilmann H.J., Maegert H.J., Gassen H.G.;
RT "Identification and Isolation of Glucose dehydrogenase genes of
RT Bacillus megaterium M1286 and their expression in Escherichia coll.,"
RL Eur. J. Biochem. 174:485-490(1988).
RN [4]
RP SEQUENCE OF 27-204.
RX MEDLINE=84004396; PubMed=6413208;
RA Ulmer W., Froschle M., Jany K.-D.;
RT "Evidence for an essential histidine residue in glucose dehydrogenase
RT from Bacillus megaterium and sequence analysis of the peptides
RT labeled with bromoacetyl pyridine,"
RL Eur. J. Biochem. 136:183-194(1983).
RN [5]
RP SEQUENCE OF 218-262.
RX MEDLINE=84285362; PubMed=6432532;
FT


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RA Froschle M., Ulmer W., Jany K.-D.;
RT "Tyrosine modification of glucose dehydrogenase from Bacillus
RT megaterium. Effect of tetranitromethane on the enzyme in the
RT tetrameric and monomeric state.";
RL Eur. J. Biochem. 142:533-540(1984).
CC -1- CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+) -> D-glucono-1,5-
CC lactone + NAD(P)H.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING SPOULATION.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR PIR: S02299; S02299.
DR PIR: S01227; S01227.
DR PIR: A20238; A20238.
DR PIR: B20238; B20238.
DR PIR: C20238; C20238.
DR PIR: D20238; D20238.
DR PIR: A23260; A23260.
DR PIR: A23260; A23260.
DR HSP: P50163; 2AEL.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NADP; Multigene family; Sporulation.
FT NP_BIND 11 35 NADP (BY SIMILARITY).
FT ACT_SITE 160 160 BY SIMILARITY.
SQ SEQUENCE 262 AA; 28347 MW; C9281328D634E789 CRC64;

Query Match 27.9%; Score 360; DB 1; Length 262;
Best Local Similarity 34.2%; Pred. No. 2.2e-22;
Matches 88; Conservative 51; Mismatches 106; Indels 12; Gaps 6;

QY 1 MSNRLOGVAITGTLGIGLAIAFKVEGAKVMIT-----DRHSDVGEKAASVGPDP 55
DB 1 MYKDLGKVVVITGSGTGLSKMAIRFATEKAKVVVYRSKEDEANSVLEEIKVG--G 58
QY 56 QIOPFQHDSDDEGWTKLFDATEKAFGVPSTLVNAGIANKSVSEETTAERKLLAVNL 115
DB 59 EATAVKGDTVESDVINLVQSAIKFEKGLDVMINNAGMENPVSSHMSLSDWKNKVIDTNL 118
QY 116 DGVEFGTRLGQRMKNKGLGASIIINMSI-EGFVGDPISLGAYNASKGAVRIMSKSAALDC 174
DB 119 TGAFLGSRKAIFYENDIKGTVINMSVHEWKPWPLFVHYAASKGMKLTETLLEY 178
QY 175 ALKDYDVRVTVHPGYIKTKPL-VDDLPGAEAMSQRTKTPMGHIGEPNDIAYICVILASN 233
DB 179 APR--GIRVNNIGPGAINTPINAEKPADPEORADVESMIPMGYIGEPEEIAAV-AWLASS 235
QY 234 ESKFATGSEFVDDGGYT 250
DB 236 EASYVTGTLTFADGGMT 252

RESULT 13
DHG_BACSU STANDARD; PRT; 261 AA.
AC P12310; P94430;
DT 01-OCT-1989 (Rel. 12, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glucose 1-dehydrogenase (EC 1.1.1.47).
GN GDH.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86168021; PubMed=3082854;
RA Lampel K.A., Uratani B., Chaudhry G.R., Ramaley R.F., Rudikoff S.;
RT "Characterization of the developmentally regulated Bacillus subtilis
RT glucose dehydrogenase gene.";
RL J. Bacteriol. 166:238-243(1986).

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(2)
RN SEQUENCE FROM N.A.
RP STRAIN=168;
RC MEDLINE=97124189; PubMed=8969502;
RA Yamane K., Kumano M., Kurita K.;
RT "The 25 degrees-36 degrees region of the Bacillus subtilis chromosome:
RT determination of the sequence of a 146 kb segment and identification
RT of 113 genes.";
RL Microbiology 142:3047-3056(1996).
CC -1- CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+) -> D-glucono-1,5-
CC lactone + NAD(P)H.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- INDUCTION: IT IS INDUCED AT STAGE III OF THE SPOULATION.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: M12276; AAA22463.1; -
DR EMBL: D50453; BAA09024.1; -
DR EMBL: Z99106; CAB12201.1; -
DR PIR: S36090; S36090.
DR HSP: P50162; 1AEL.
DR Subtilisin; BGI0545; gdh.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NADP; Sporulation; Complete proteome.
FT NP_BIND 11 35 NADP (BY SIMILARITY).
FT ACT_SITE 158 158 BY SIMILARITY.
FT CONFLICT 148 150 EVI -> AF (IN REF. 1).
SQ SEQUENCE 261 AA; 28090 MW; 5894C17DB8F14965 CRC64;

Query Match 27.8%; Score 358.5; DB 1; Length 261;
Best Local Similarity 33.9%; Pred. No. 2.8e-22;
Matches 87; Conservative 45; Mismatches 104; Indels 21; Gaps 5;

QY 5 LDGKVAITGTLGIGLAIAFKVEGAKVMIT-----DRHSDVGEKAASVGPDPQIQF 59
DB 5 LKGVVAITGAASGLGKMAIRFGEQAKVVVINYSKQDPNEKVEIKAGG---EAVV 61
QY 60 FQHDSDDEGWTKLFDATEKAFGVPSTLVNAGIANKSVSEETTAERKLLAVNLGVF 119
DB 62 VQGDVTKREDVKNIQVTAIRKEFGTLDIMINNAGLENVPVSHENPLKDKDKVIGTNLGF 121
QY 120 FGRRLGQRMKNKGLGASIIINMSIEFGVDPISLGAYNASKGAVRIMSKSAALCALDY 179
DB 122 LGSREAIKIFYENDIKGTVINMSVHEWKPWPLFVHYAASKGKIKLTETLLEYAPK-- 179
QY 180 DVRTVTVHPGYIKTKPLVDDLPGAEAMSQRTK-----PMGHIGEPNDIAYICVILASN 233
DB 180 GIRVNNIGPGAINTPI-----NAEKFPADPKOKADVESMIPMGYIGEPEEIAAVAWLASK 234
QY 234 ESKFATGSEFVDDGGYT 250
DB 235 EASYVTGTLTFADGGMT 251

RESULT 14
DHG4_BACME STANDARD; PRT; 261 AA.
ID DHG4_BACME
AC P39485;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Glucose 1-dehydrogenase IV (EC 1.1.1.47) (GLCDH-IV).

```


GN DHIV.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-IAM 1030;
RA Nagao T., Mitamura T., Wang X.H., Negoro S., Yomo T., Urabe I.,
Okada H.;
RT Cloning, nucleotide sequences, and enzymatic properties of glucose
dehydrogenase isozymes from Bacillus megaterium IAM1030.*;
RL J. Bacteriol. 174:5013-5020(1992).
CC -|- CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+) -> D-glucono-1,5-
lactone + NAD(P)H.
CC -|- SUBUNIT: HOMOTETRAMER.
CC -|- MISCELLANEOUS: PREFERENCES NAD TO NADP; 2M NaCl ENHANCES ITS PH AND
THERMOSTABILITY.
CC -|- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
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CC
DR EMBL; D10626; BAA01476.1;
DR HSP; P50162; IAE1.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NAD; Multigene family.
FT NP_BIND 11 35 NAD (BY SIMILARITY).
FT ACT_SITE 158 158 BY SIMILARITY.
SQ SEQUENCE 261 AA; 28157 MW; 6PBEC9397BCF417C CRC64;

Query Match 27.7%; Score 357.5; DB 1; Length 261;
Best Local Similarity 32.1%; Pred. No. 3.4e-22;
Matches 85; Conservative 51; Mismatches 100; Indels 29; Gaps 6;

QY 1 MSNRLDGKVAITGGTGLGIGLAIAIKFVEEGAKVMT-----DRHSDVGERAAKSV 51
DB 1 MTYDLKDKVVVITGGTGLGRAMAVRFQGEAKVINYNNNEEALDAKVEEAGGQAI 60

QY 52 GTPDQIQFQHDSSDEGWTKLFDATKAFGPVSTLVNNAIYVNSVETTTAEWRKLL 111
DB 61 -----IVQGDVTKEDVNVLVQTAKEFGTLDVNNAGVENPVPSHELSDNNKVI 113

QY 112 AVNLDGVFGTGLGIQRMKNKGLGASINMSIEGFDGDPSPGAYNASKGAVRIMSKSA 171
DB 114 DNLGAFGLSREAIKYFVENDIKGNVINSSVHEMIPWPLFVHYAASKGGMKLTETLA 173

QY 172 LDCALKDYRVNTVHPGYIKTPL-----VDLPGAE-EAMSQRTKTPMGHIGEPNDIAY 225
DB 174 LEYAPK--GIRVNNIGPGAMTPINAEKFPADVPQRADVESM-----IPMGYIGKPEEVA 226

QY 226 ICYLLASNEKFCATGSEFYVDGGYT 250
DB 227 VAAFLASSQASVVTGTTLPADGGMT 251

RESULT 15
DHG2_BACME STANDARD; PRT; 261 AA.
AC P39483;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Glucose 1-dehydrogenase II (EC 1.1.1.47) (GLCDH-II).
GN GDHII.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-IAM 1030;
RA Mitamura T., Ebara R.V., Nakai T., Makino Y., Negoro S., Urabe I.,
Okada H.;
RT *Structure of isozyme genes of glucose dehydrogenase from Bacillus
megaterium IAM1030.*;
RL J. Ferment. Bioeng. 70:363-369(1990).
CC -|- CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+) -> D-glucono-1,5-
lactone + NAD(P)H.
CC -|- SUBUNIT: HOMOTETRAMER.
CC -|- MISCELLANEOUS: PREFERENCES NADP TO NAD.
CC -|- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
CC
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CC
DR EMBL; D90044; BAA14100.1;
DR HSP; P50162; IAE1.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NADP; Multigene family.
FT NP_BIND 11 35 NADP (BY SIMILARITY).
FT ACT_SITE 158 158 BY SIMILARITY.
SQ SEQUENCE 261 AA; 28251 MW; CEF9AA1425D2999C CRC64;

Query Match 27.6%; Score 355.5; DB 1; Length 261;
Best Local Similarity 31.4%; Pred. No. 5e-22;
Matches 80; Conservative 55; Mismatches 111; Indels 9; Gaps 4;

QY 1 MSNRLDGKVAITGGTGLGIGLAIAIKFVEEGAKVMTDRHSDVG-----EKAASVCTPQ 56
DB 1 MTYDLKDKVVVITGGTGLGRAMAVRFQGEAKVINYNNNEEALDAKVEEAG--GQ 58

QY 57 IQFFQHDSSDEGWTKLFDATKAFGPVSTLVNNAIYVNSVETTTAEWRKLLAVNLD 116
DB 59 AIIVRGDVTKEEDVNVLVQTAKEFGTLDVNNAGVENPVPSHELSDNNKVI 118

QY 117 GVFFGTRIGIQRMKNGKGLGASINMSIEGFDGDPSPGAYNASKGAVRIMSKSAALDCA 176
DB 119 GAFLGSREAIKYFVENDIKGNVINSSVHEMIPWPLFVHYAASKGGMKLTETLALEYAP 178

QY 177 KYDVRVNTVHPGYIKTPL--VDLPGAE-EAMSQRTKTPMGHIGEPNDIAYICVYLASNE 235
DB 179 K--GIRVNNIGPGAMTPINAEKFPADVPQRADVESMIPMGYIGKPEEIASVAAPLASSQA 236

QY 236 KFATGSEFYVDGGYT 250
DB 237 SVVTGTTLPADGGMT 251

Search completed: October 30, 2002, 15:45:26
Job time : 14 secs

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OM protein - protein search, using sw model

Run on: October 30, 2002, 15:45:05 ; Search time 27 Seconds
(without alignments)
1614.619 Million cell updates/sec

Title: US-09-910-033a-2
Perfect score: 1290
Sequence: 1 MSNRLDGKVAITGTLGIG.....NESKFGTCSEFVDDGGVTAQ 252

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_19:**
- 1: sp_archaea:**
 - 2: sp_bacteria:**
 - 3: sp_fungi:**
 - 4: sp_human:**
 - 5: sp_invertebrate:**
 - 6: sp_mammal:**
 - 7: sp_mhc:**
 - 8: sp_organelle:**
 - 9: sp_phase:**
 - 10: sp_plant:**
 - 11: sp_rodent:**
 - 12: sp_virus:**
 - 13: sp_vertebrate:**
 - 14: sp_unclassified:**
 - 15: sp_rvirus:**
 - 16: sp_bacteriap:**
 - 17: sp_archaeap:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	470	36.4	261	16	Q9AB11	Q9ab11 caulobacter
2	452.5	35.1	250	2	Q937L4	Q937L4 conamonas t
3	438	34.0	254	2	Q9K4G9	Q9K4G9 streptomyce
4	411	31.9	251	2	Q9RNK5	Q9rnk5 zymomonas m
5	411	31.9	254	2	Q52587	Q52587 conamonas t
6	395.5	30.7	256	2	Q93QG5	Q93qg5 brevivibacter
7	391	30.3	249	2	Q56841	Q56841 xanthobacte
8	386.5	30.0	247	2	Q93RM0	Q93rm0 acinetobact
9	386.5	30.0	251	2	Q9F7E0	Q9f7e0 acinetobact
10	378.5	29.3	258	2	Q9JN17	Q9jnl7 agrobacteri
11	376.5	29.2	255	16	Q98EN0	Q98en0 rhizobium l
12	374.5	29.0	248	16	Q31680	Q31680 bacillus su
13	374.5	29.0	250	16	Q98C63	Q98c63 rhizobium l
14	373	28.9	249	2	Q9LBC5	Q9lbg5 geobacillus m
15	372.5	28.9	253	16	Q930L7	Q930l7 rhizobium m
16	370	28.7	246	2	Q9EX74	Q9ex74 rhodococcus

17	369.5	28.6	251	16	Q92PX8	Q92px8 rhizobium m
18	368	28.5	253	16	Q9CH41	Q9ch41 lactococcus
19	367	28.4	258	16	Q33339	Q33339 mycobacteri
20	366	28.4	272	16	Q99RG1	Q99rg1 staphylococ
21	364.5	28.3	255	16	P95286	P95286 mycobacteri
22	364	28.2	264	2	Q9AK65	Q9ak65 streptomyce
23	360	27.9	251	2	Q9FDK2	Q9fdk2 zymomonas m
24	359	27.8	256	16	Q982N5	Q982n5 rhizobium l
25	358	27.8	270	6	Q9WVP6	Q9wvp6 bos taurus
26	357.5	27.7	258	16	Q930L5	Q930l5 rhizobium m
27	357.5	27.7	261	2	Q9F5L5	Q9f5l5 bacillus su
28	357	27.7	296	16	Q9ABX6	Q9abx6 caulobacter
29	356.5	27.6	256	16	Q92MR3	Q92mr3 rhizobium m
30	351	27.2	286	16	Q911X3	Q911x3 pseudomonas
31	350	27.1	257	16	Q9WYD3	Q9wyd3 thermotoga
32	348.5	27.0	255	16	Q92RW7	Q92rw7 rhizobium m
33	347.5	26.9	268	17	Q9HLN6	Q9hln6 thermoplasm
34	347	26.9	243	16	Q9KCO9	Q9kcg9 bacillus ha
35	346.5	26.9	254	2	Q9RH24	Q9rh24 zymomonas m
36	346.5	26.9	255	16	Q9WYS2	Q9wys2 thermotoga
37	346.5	26.9	268	16	Q986J1	Q986j1 rhizobium l
38	346	26.8	248	2	Q923Y5	Q923y5 pseudomonas
39	345.5	26.8	261	2	Q9F2A6	Q9f2a6 bacillus l
40	345	26.7	248	16	Q987H1	Q987h1 rhizobium l
41	344.5	26.7	261	17	Q97CM7	Q97cm7 thermoplasm
42	344	26.7	303	10	Q9SCU0	Q9scu0 arabidopsis
43	343.5	26.6	250	2	Q56840	Q56840 xanthobacte
44	343.5	26.6	299	17	Q97UR6	Q97uk6 sulfobolus
45	343	26.6	255	17	Q9HK51	Q9hk51 thermoplasm

ALIGNMENTS

RESULT 1

Q9AB11	PRELIMINARY;	PRT;	261 AA.
ID Q9AB11			
AC Q9AB11			
DT 01-JUN-2001 (TREMREL. 17, Created)			
DT 01-JUN-2001 (TREMREL. 17, Last sequence update)			
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)			
DE 2,5-DICHLORO-2,5-CYCLOHEXADIENE-1,4-DIOL DEHYDROGENASE.			
GN CC0246.			
OS Caulobacter crescentus.			
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;			
OC Caulobacter.			
OX NCBI_TaxID=69394;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=ATCC 19089 / CB15;			
RX MEDLINE=21173698; Pubmed=11259647;			
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kollonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;			
RT "Complete genome sequence of Caulobacter crescentus."			
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).			
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.			
DR EMBL; AE005698; AAK22233.1; -			
DR HSSP; P19992; LHDC.			
DR TIGR; CC0246; -			
DR InterPro; IPR002198; ADH_short.			
DR Pfam; PF00106; adh_short; 1.			
DR PRINTS; PS00080; SDRFAMILY.			
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.			
KW Complete proteome; Oxidoreductase.			
SQ SEQUENCE 261 AA; 27011 MW; CE011D872D4EBA6D CRC64;			

Query Match 36.4%; Score 470; DB 16; Length 261;

DE	BETA-HYDROXYSTEROID DEHYDROGENASE.
OS	Zymomonas mobilis.
OC	Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
OX	Zymomonas.
ON	NCBI_TaxID=542;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-ZM4;
RA	Lee H.J., Kang H.S.;
RT	*Sequence analysis of 42F4 fosmid clone of Zymomonas mobilis ZM4.*;
RL	Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
CC	-1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
DR	EMBL; AF180145; AAD56922.1; -.
DR	HSSP; PI19992; LHDC.
DR	InterPro; IPR002198; ADH_short.
DR	Pfam; PF00106; adh_short; 1.
DR	PRINTS; PR00080; SDRFAMILY.
KW	Oxidoreductase.
SQ	SEQUENCE 251 AA; 26621 MW; 62DDI51CAFA7CF6B CRC64;

Query Match	31.9%; Score 411; DB 2; Length 251;
Best Local Similarity	40.6%; Pred. No. 2.le-23;
Matches 101; Conservative 33; Mismatches 95; Indels 20; Gaps	

Qy	14	GGTGIGLATATKVFEGAKVMIDRISDVGEKAASVGTDPQIQFFQHDSSDEDGWTKL	73
Dd	1	: :	: : : :
Dd	5	GCARGIGRAIAAFQHKGAKVIIVTDIDEVTGCKTAAEITGG---QFOKLDVREEKWQL	60
Qy	74	FDATEKAFGPVSTLVNNAGI-----AVNKSVETTTAEWRKKLLAVNLGDGVFFGTRLGIO	127
Dd	61	AETVP-----VDVVNNAGITGFENGVAHDPEHATLEDMDRAVRVNLDGFCGLCRYAIA	116
Qy	128	RMKNKGIGASIIINMSISIEGFGDPSLAGYNASKGAVRIMSKSAALDCAIKDYDVRVNTVH	187
Dd	117	AMNKGKG-SIINISSRSLGVGIPLAAYASSKAAIRNHKSVALYCAQQGWKTRCHNAIN	175
Qy	188	PGYIKTPLVDDLPGAEEAMSGTK-----TPMGHIGEPNDIAYTCVLASNESKFATGSE	242
Dd	176	PAALTSIWEPMLGDGDDRKRMOALVADTPLKRFGLPEEVAAVAVMASDEATYMTGAEE	235
Qy	243	FVVDGGYTA 251	
Dd	236	FNIDGGLLA 244	

RESULT 5	PRELIMINARY; PRT; 254 AA.
Q52587	
ID	Q52587
AC	Q52587
DT	01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	BETA-HYDROXYSTEROID DEHYDROGENASE.
OS	Comamonas testosteroni (Pseudomonas testoteroni).
OC	Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
ON	NCBI_TaxID=285;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-ATCC 11996;
RA	Cabrera J.E., Gentil-Raimondi S.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC	-1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
DR	EMBL; U41265; AAA25742.1; -.
DR	HSSP; PI19992; LHDC.
DR	InterPro; IPR002198; ADH_short.
DR	Pfam; PF00106; adh_short; 1.
DR	PRINTS; PR00080; SDRFAMILY.
DR	PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
KW	Oxidoreductase.
SQ	SEQUENCE 254 AA; 26952 MW; FB6EC90B151975DB CRC64;

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RESULT 7
O56841
ID Q56841 PRELIMINARY; PRT; 249 AA.
AC Q56841;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ORF5 PROTEIN.
GN ORF5.
OS Xanthobacter sp.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae group; Xanthobacter.
OX NCBI_TaxID=35809;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PY2;
RX MEDLINE=95219103; PubMed=7704278;
RA Swaving J., Weljers C.A.G.M., van Ooyen A.J.J., de Bont J.A.M.;
RT "Complementation of Xanthobacter Py2 mutants in epoxylane
RT degradation; expression and nucleotide sequence of the complementing
RT DNA fragment.";
RL Microbiology 141:477-484(1995).
RC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; X79863; CAAS56245.1; -.
DR HSSP; P19992; LHDC.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PRO0080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
KW Oxidoreductase.
SQ SEQUENCE 249 AA; 24940 MW; B5E0B82C1D8D9782 CRC64;

Query Match 30.3%; Score 391; DB 2; Length 249;
Best Local Similarity 38.9%; Pred. No. 6.6e-22;
Matches 98; Conservative 39; Mismatches 105; Indels 10; Gaps 6;

QY 5 LQKVAITGGTIGIGLAITATKVEGAKVMTDRHSVDGGEKAASVGTDPQIQFQHDS 64
DB 2 LQAEVITGGAGIGLAIAHAAIRAGARVALIDRDGACAAQRAAEFGA--AAWGVGADV 59

QY 65 SDEGHTKLFDATEKAFGPVSTLVNAGAVNKSVEETTTAEWRKLLAVNLDGVFGTRL 124
DB 60 TDEAATAMAGAAQALGPLTGLVNNAGIAGFGSVHATEVETWSRIMAVNVVTGTFLLASKA 119

QY 125 GIORMKNKGLGASIIINSSIEGFGVDPGSLGAYNASKGAVRIMSKSAALDCALXDYVRVN 184
DB 120 ALPGMLERGRGA-IVNFGSVAGLVGIPITMAAYCAKAGAVNLTROMADYSGR--GIRVN 176

QY 185 TVHPGVYIK-TPLVDDLPFAE--EAMSOR-TKTPMGHIGEPNDIAYICVYLASNEKFA 239
DB 177 VVCPGVVAGTDMGROLGLTDCDPELEARRLAKYPMGRFGTTPEDIAEAAYFLLSTKAAFT 236

QY 240 GSEFVDDGCGYTA 251
DB 237 GSVLAVDGGHTA 248

RESULT 8
O93RMO
ID Q93RMO PRELIMINARY; PRT; 247 AA.
AC Q93RMO;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE CYCLOHEXANOL DEHYDROGENASE.
GN CHNA.
OS Acinetobacter sp. NCIMB9871.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC Acinetobacter.
OX NCBI_TaxID=93373;
RN [1]
RP SEQUENCE FROM N.A.

Query Match 30.0%; Score 386.5; DB 2; Length 251;
Best Local Similarity 33.7%; Pred. No. 1.5e-21;
Matches 86; Conservative 60; Mismatches 98; Indels 11; Gaps 6;

QY 1 MSNRLDGKVAITGGTIGIGLAITATKVEGAKVMTDRHSVDGGEKA--KSVGTPDQIQF 59
DB 5 MSNKNKVALITGAGSGIGKSTALLLAQOGVSVVSDINLEAAQKVVDI VALGKAAA 64

QY 60 FQHDSSDEGWTKLFDATEKAFGPVSTLVNAGI--AVNKSVEETTTAEWRKLLAVNLDG 117
DB 60 FQHDSSDEGWTKLFDATEKAFGPVSTLVNAGI--AVNKSVEETTTAEWRKLLAVNLDG 117

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RC STRAIN=NCIMB 9871;
RA Iwaki H., Hasegawa Y., Teraoka M., Tokuyama T., Lau P.C.;
RT "Identification and Characterization of Cyclohexanol Metabolic Genes
RT from Acinetobacter sp. NCIMB 9871.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB026668; BAB61742.1; -.
SQ SEQUENCE 247 AA; 25657 MW; AB0DA7904DE726B3 CRC64;

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Query Match 30.0%; Score 386.5; DB 2; Length 247;
Best Local Similarity 33.7%; Pred. No. 1.4e-21;
Matches 86; Conservative 60; Mismatches 98; Indels 11; Gaps 6;

QY 1 MSNRLDGKVAITGGTIGIGLAITATKVEGAKVMTDRHSVDGGEKA--KSVGTPDQIQF 59
DB 1 MSNKNKVALITGAGSGIGKSTALLLAQOGVSVVSDINLEAAQKVVDI VALGKAAA 60

QY 60 FQHDSSDEGWTKLFDATEKAFGPVSTLVNAGI--AVNKSVEETTTAEWRKLLAVNLDG 117
DB 60 FQHDSSDEGWTKLFDATEKAFGPVSTLVNAGI--AVNKSVEETTTAEWRKLLAVNLDG 117
DB 61 NKANTAEPEDKAAVEFAVSTFGALHLAFNAGILGEVN-STEEISTEGWRRVIDVNLNA 119
QY 118 VFETRLGIQRMKNKGLGASIIINSSIEGFGVDPGSLGAYNASKGAVRIMSKSAALDCALX 177
DB 120 -VFSMHEVPAIILAAG-GGAIVNTASIALGIGIONISGYVAARKHGVTLTKRAALEYA-- 176

QY 178 DYDVRVNTVHPGYIKTPLVDDLPFAEEMSORTKTPMGHIGEPNDIAYICVYLASNEKSF 237
DB 177 DKGIRINSVHPGYIKTPLIAEFEEAEEMVKLH---PIGRIGQPPEAAVAVFLLSDDAF 232

QY 238 ATGSEFVDDGCGYTAQ 252
DB 233 VTGSQVVDGAYTSK 247

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RESULT 9
O9F7E0
ID Q9F7E0 PRELIMINARY; PRT; 251 AA.
AC Q9F7E0;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE CYCLOHEXANOL DEHYDROGENASE.
GN CHNA.
OS Acinetobacter sp. SE19.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC Acinetobacter.
OX NCBI_TaxID=135835;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SE19;
RX MEDLINE=20398154; PubMed=10940013;
RA Cheng Q., Thomas S.M., Kostichka K., Valentine J.R., Nagarajan V.;
RT "Genetic analysis of a gene cluster for cyclohexanol oxidation in
RT acinetobacter sp. strain SE19 by in vitro transposition.";
RL J. Bacteriol. 182:4744-4751(2000).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AF282240; AAG10026.1; -.
DR HSSP; P19992; LHDC.
DR InterPro; IPR002198; ADH_short.
DR PRINTS; PRO0080; SDRFAMILY.
KW Oxidoreductase.
SQ SEQUENCE 251 AA; 26159 MW; B5BAA48055997D5D CRC64;

```

```

Query Match 30.0%; Score 386.5; DB 2; Length 251;
Best Local Similarity 33.7%; Pred. No. 1.5e-21;
Matches 86; Conservative 60; Mismatches 98; Indels 11; Gaps 6;

QY 1 MSNRLDGKVAITGGTIGIGLAITATKVEGAKVMTDRHSVDGGEKA--KSVGTPDQIQF 59
DB 5 MSNKNKVALITGAGSGIGKSTALLLAQOGVSVVSDINLEAAQKVVDI VALGKAAA 64

QY 60 FQHDSSDEGWTKLFDATEKAFGPVSTLVNAGI--AVNKSVEETTTAEWRKLLAVNLDG 117
DB 60 FQHDSSDEGWTKLFDATEKAFGPVSTLVNAGI--AVNKSVEETTTAEWRKLLAVNLDG 117

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Db 65 NKANTAEPEDKAAVEFAVSTGALHLAFNNAGILGEVN-STEELSIEGWRVIDVNLNA 123
Qy 118 VFGTRGLQRMKNKGLGASIIINSSIEGFGVDPSPSLGAYNASKGAVRIMSKSAALDCALK 177
Db 124 VFSYMHYEPAILAAG-GGAIVNTASIAGLIGIONISGVAAKHGVTGLTKAAALEYA-- 180
Qy 178 DYDVRVNTVHPGYIKTPTLVDDLPGLGAEAMSQRTKTPMGHIGEPNDIAYICVILASNEKF 237
Db 181 DKGIRINSVHPGYIKTPTLVDDLPGLGAEAMVRLH---PIGLGQPEEVAQVAFLLSDAS 236
Qy 238 ATGSEFVVDGYTAQ 252
Db 237 VTGSQVVDGYTSK 251

RESULT 10
Q9JN17 PRELIMINARY; PRT; 258 AA.
AC Q9JN17 (TREMREL. 15, Created)
DT 01-OCT-2000 (TREMREL. 15, Last sequence update)
DE 01-OCT-2000 (TREMREL. 15, Last sequence update)
DE 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE YHG.
GN YHG.
OS Agrobacterium tumefaciens.
OG Plasmid T1.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=358;
RN [1]
RP SEQUENCE OF 1-6 FROM N.A.
RX MEDLINE=96236046; PubMed=8655509;
RA Kim K.S., Farrand S.K.;
RT "Ti plasmid-encoded genes responsible for catabolism of the crown gall
RT opine mannopine by Agrobacterium tumefaciens are homologs of the T-
RT region genes responsible for synthesis of this opine by the plant
RT tumor."
RL J. Bacteriol. 178:3275-3284(1996).
RN [2]
RP SEQUENCE OF 4-258 FROM N.A.
RX MEDLINE=99141607; PubMed=9987134;
RA Lyi S.M., Jafri S., Winans S.C.;
RT "Mannopine acid and agropinonic acid catabolism region of the octopine-
RT type Ti plasmid pTi15955."
RL Mol. Microbiol. 31:339-347(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Winans S.C., Zhu J., Oger P.M., Schrammeijer B., Hooykaas P.J.,
RA Farrand S.K.;
RT "Octopine-type Ti plasmid sequence."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AF242881; AAF77146.1; --
DR HSPF; P50162; IAE1.
DR InterPro; IPR002198; ADH_short.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
KW Oxidoreductase; plasmid.
SQ SEQUENCE 258 AA; 27591 MW; B4E4D0364468C44C CRC64;

Query Match 29.3%; Score 378.5; DB 2; Length 258;
Best Local Similarity 37.6%; Pred. No. 6.1e-21;
Matches 97; Conservative 40; Mismatches 102; Indels 19; Gaps 6;

Qy 4 RLDGKVAITGTGTLGIGLAIAATKFEVEGAKVMITDRHSDVGEKAASVGTPTDQIOFFOHD 63
Db 11 RLDGKVAITGTGTLGIGLAIAATKFEVEGAKVMITDRHSDVGEKAASVGTPTDQIOFFOHD 69
Qy 64 SDEGWTKLDATEKAFGPVSTLVNAGIAVKNKSVEETTTAEVRKLLAVNLDGVFGTR 123
Db 70 LKTRACALVKKRVADDRGLDILINAGIANGDTPLFTQQWRDVIATNVTETVWCQS 129

Qy 124 LGIQRMKNKGLGASIIINSSIEGFGVD--PSLGAYNASKGAVRIMSKSAALDCALKDYDV 181
Db 130 AAIPVMEGRGA-IVNYSMSGIVSNIPQNVAYNSSKAAVHMTKSLASELALD--NI 186
Qy 182 RVNTHVHPGYIKTPTLVDDLPGLGAEAMSQRTK-----TPMGHIGEPNDIAYICVILASNE 234
Db 187 RVNTHVHPGYIKTPTLVDDLPGLGAEAMVRLH---PIGLGQPEEVAQVAFLLSDAS 240
Qy 235 SKFATGSEFVVDGYTAQ 252
Db 241 SSYVTGDIIVDGGYTR 258
RESULT 11
Q98EN0 PRELIMINARY; PRT; 255 AA.
AC Q98EN0;
DT 01-OCT-2001 (TREMREL. 18, Created)
DT 01-OCT-2001 (TREMREL. 18, Last sequence update)
DE 01-OCT-2001 (TREMREL. 18, Last annotation update)
DE SHORT-CHAIN DEHYDROGENASE.
GN MLR4172.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti."
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003003; BAB50888.1; --
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
KW Complete proteome.
SQ SEQUENCE 255 AA; 26441 MW; 7EAF89BB46810117 CRC64;

Query Match 29.2%; Score 376.5; DB 16; Length 255;
Best Local Similarity 38.3%; Pred. No. 8.4e-21;
Matches 101; Conservative 37; Mismatches 103; Indels 23; Gaps 7;

Qy 1 MSNRLDGRVAITGTGTLGIGLAIAATKFEVEGAKVMITDRHSDVGEKAASVGTPTDQI-QF 59
Db 1 MGERLAGVAISGGATCGMGNASELFPAEGAKVAIIDRNGEAAAATAAAIRARGEVAEH 60
Qy 60 FOHDSDE-DGWTKLDATEKAFGPVSTLVNAGIAVKNKSVEETTTAEVRKLLAVNLDGV 118
Db 61 FVADVSDEAQVAAVKGATEK-LGPVTVLFNHAGTVIKPFLETTQVQEWDLHAVNVRSM 119
Qy 119 FFGRLGIRQMKNGKLGASIIINSSIEGFGVDPSPSLGAYNASKGAVRIMSKSAALDCALKD 178
Db 120 FLMTAVLPGVMIAG-GGSIVCTSSISAVAAPTPMEVLYDTRKGACHMFARAI-AVE--FRD 176
Qy 179 YDVRVNTVHPGYIKTPTLVDDLPGLGAEAMSQRTKTPMGHIGEPNDIAYIC 227
Db 177 RNIRCNVCPGFIRTPHGLREVADLGLKGLGVDSDAALAAQ-----GRIGEPPEVAKAA 230
Qy 238 VYLASNESKFATGSEFVVDGYTA 251
Db 231 LYLASDESSFVNGAHLFVDNGFTA 254

RESULT 12
Q31680 PRELIMINARY; PRT; 248 AA.
ID Q31680

O31680;
 01-JAN-1998 (TREMBLrel. 05, Created)
 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE YKVO PROTEIN.
 GN YKVO.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 SEQUENCE FROM N.A.
 STRAIN=168;
 MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 Borriass R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
 Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 Fritz C., Fujita M., Fujita Y., Fuma S., Gallizzi A., Galleron N.,
 Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
 Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 Parro T., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 Prescan E., Pujic P., Purnelle B., Porwollik S., Prescott A.M.,
 Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
 Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
 Sorokin A., Tacconi A., Takagi T., Takahashi H., Takemaru K.,
 Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 Viarri A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the gram-positive bacterium Bacillus
 subtilis."
 RL Nature 390:249-256(1997).
 RN [2]
 SEQUENCE FROM N.A.
 STRAIN=168;
 RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDR) FAMILY.
 DR EMBL; Z99111; CAB13250.1; -;
 DR HSP; P47227; 1BD8.
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 KW Complete proteome; Oxidoreductase.
 SQ SEQUENCE 248 AA; 26245 MW; EACA490C1239524D CRC64;
 Query Match 29.0%; Score 374.5; DB 16; Length 248;
 Best Local Similarity 37.5%; Pred. No. 1.2e-20;
 Matches 93; Conservative 40; Mismatches 106; Indels 9; Gaps 5;
 QY 4 RLDGKVAITGGTGLGIGLAIAATKFEVGEAKVMTDRHSVDGGEAKAASVGPDPQIQFQHD 63
 DB 3 KFEGLAVITGGTSGIGLATAQKFEVNEGAVVITGRQNELDKAVNIG--KNVTGVQGD 60
 QY 64 SDEDGWTGLFDATEKAFGPVSTLVNNAIVNKSVEETTTAEWRKLLAVNLGVPFGTR 123
 DB 61 ISKLEDLKLVDIIRKQEKGLDLIFANAGIGNFLPLGEITEEQVDRTFDINVKGTFTTQ 120
 QY 124 LGTQRMKNGKGLASIIINMSIEGFGVDPSPISLAYNASKGAVRIMSKSAALDCAKLDYDVRV 183
 DB 121 KALPLFKD---GGSIILNSSVNVGLPGFSTYAAKAAVRNFSRAWTLE--LKDKIRV 175
 QY 184 NTVHPGIYTKPLVDDLPG-----AEEAMSO-RRTKTPMGHIGEPNDIAYICVYLASNESKF 237
 DB 176 NMSPGAIEITPALETITGLTPEQAQVAQAFASQIPWRRGKPEETIAAAVTFASDDSSY 235
 QY 238 ATGSEFVDDG 248
 DB 236 VTGVDLAVDGG 246

Db 121 KALSFPDK--VGSIIVTGSTAGSIGNPAFSVYGASKAALRALVRNWILD--LKGEIRV 176
 QY 184 NTVHPGIYTKPLVDDLPG--AEEAM-SORTKTPMGHIGEPNDIAYICVYLASNESKFATG 240
 DB 177 NVSPGGILTPAYDELFGDALEEVLENSRNTVPAGKVTPEEVANAVSFASDESSYLTG 236
 QY 241 SEFVDDG 248
 DB 237 VELFVDDG 244
 RESULT 13
 Q98C63
 ID Q98C63 PRELIMINARY; PRT; 250 AA.
 AC Q98C63;
 DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 DE GLUCOSE DEHYDROGENASE.
 GN MLE5280.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 SEQUENCE FROM N.A.
 STRAIN=MAFF303099;
 RC MEDLINE=21082930; PubMed=11214968;
 RX Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 Watanabe A., Iidesawa K., Ishikawa A., Kawashima K., Kimura T.,
 Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 Takeuchi C., Yamada M., Tabata S.;
 RA "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti."
 RT DNA Res. 7:331-338(2000).
 RL EMBL; AP003006; BAB51758.1; -;
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 KW Complete proteome.
 SQ SEQUENCE 250 AA; 26407 MW; 1736D8C3F6711274 CRC64;
 Query Match 29.0%; Score 374.5; DB 16; Length 250;
 Best Local Similarity 37.1%; Pred. No. 1.2e-20;
 Matches 93; Conservative 47; Mismatches 98; Indels 13; Gaps 5;
 QY 4 RLDGKVAITGGTGLGIGLAIAATKFEVGEAKVMTDRHSVDGGEAKAASVGPDPQIQFQHD 63
 DB 3 KLEKIAVITGGSGIGLATAKRFVEGAHVITGRREKELKEAAFI--MRNVTTVGD 60
 QY 64 SDEDGWTGLFDATEKAFGPVSTLVNNAIVNKSVEETTTAEWRKLLAVNLGVPFGTR 123
 DB 61 VSLEDLDRIVAVVKEKHGHDIVLFANAGAGTAPLAAATEAHFDQTFDYNKGLFTTQ 120
 QY 124 LGTQRMKNGKGLASIIINMSIEGFGVDPSPISLAYNASKGAVRIMSKSAALDCAKLDYDVRV 183
 DB 121 KALPLFKD---GGSIILNSSVNVGLPGFSTYAAKAAVRNFSRAWTLE--LKDKIRV 175
 QY 184 NTVHPGIYTKPLVDDLPG-----AEEAMSO-RRTKTPMGHIGEPNDIAYICVYLASNESKF 237
 DB 176 NMSPGAIEITPALETITGLTPEQAQVAQAFASQIPWRRGKPEETIAAAVTFASDDSSY 235
 QY 238 ATGSEFVDDG 248
 DB 236 VTGVDLAVDGG 246
 RESULT 14
 Q9LBS5
 ID Q9LBS5 PRELIMINARY; PRT; 249 AA.
 AC Q9LBS5;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SHORT CHAIN ALCOHOL DEHYDROGENASE.
GN BT-ADH.
OS Geobacillus thermoleovorans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Geobacillus.
OX NCBI_TaxID=33941;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B23;
RA Morikawa M., Kanaya S., Kato T.;
RT "Short chain alcohol dehydrogenase of Bacillus thermoleovorans B23.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC -1- SIMILARITY: BELONGS TO THE EMBL-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AB040809; BAA94092.1; --.
DR HSSP; P19992; IHDC.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR002025; NAD_binding.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
KW Oxidoreductase.
SQ SEQUENCE 249 AA; 27197 MW; 072BB0DF7C6CEA31 CRC64;

Query Match 28.9%; Score 373; DB 2; Length 249;
Best Local Similarity 34.5%; Pred. No. 1.5e-20;
Matches 90; Conservative 42; Mismatches 93; Indels 36; Gaps 5;

QY 5 LQKVAITGGTIGLIGLATATKFEVGAKVMITDRSDVGEKAASVGTQDQFFQHDH 64
DB 3 IEQTAIVTGGANGIKATAPAFKOGANVVIIDRIQNGEAFAP-----QLQ----- 50

QY 65 SDESGWTKLFDATE-----KAFGPVSTLVNNAAGIYVKNKSVETTTAEWRK 109
DB 51 --SDGEALFVAADVVRKVDIERFVQEAAGRFRIDYLLNNAAGVSRKSPYELTVEEDD 108

QY 110 LLAVNLGDFVFFGTRGLGIQRMKNKGLGASIISSIEGFVGDPSLGAYNASKGAVRIMSKS 169
DB 109 VLSTNLRSFAFFASREAAKYMRNNAKGAIVNIASTRALNSEPSEAYAAKSGGLVAMTHA 168

QY 170 AALDCALKDYVRVNTVHPGYIKTPLVDDLPGAEEAMSORTKTPMGHIGEPNDIAYICVY 229
DB 169 LAVSFA--DDRIRVNCISPGWIEGTGYGLRDID-----HRQHPAGRVGKPPDIARACLY 221

QY 230 LASNESKATGSEFVVDGGYT 250
DB 222 LCDEENDFITGVNLVIDGGMT 242

RESULT 15
Q930L7 PRELIMINARY; PRT; 253 AA.
AC Q930L7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE PUTATIVE.
GN SMA0329.
OS Rhizobium melliloti (Sinorhizobium melliloti).
OG Plasmid pSymA (megaplasmid 1).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396509; PubMed=11481432;
RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;

*Nucleotide sequence and predicted functions of the entire
RT Sinorhizobium melliloti pSymA megaplasmid.*;
RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
DR EMBL; AE007211; AAK64836.1; --.
KW Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 253 AA; 26153 MW; CD0214316BA99EEF CRC64;

Query Match 28.9%; Score 372.5; DB 16; Length 253;
Best Local Similarity 37.7%; Pred. No. 1.7e-20;
Matches 97; Conservative 46; Mismatches 93; Indels 21; Gaps 8;

QY 1 MSNRLDGKVAITGGTIGLIGLATATKFEVGAKVMITDRH-----SDVGEKAASVGTDPDQ 56
DB 1 MSKRFDGKVAITGGGGSGIGAAIANRLLLEGASVYMSGRTEKRLSDVASKM-----PADR 55

QY 57 IQFFQHDSSDEDEWTKLFDATEKAFGPVSTLVNNAAGIYVKNKSVETTTAEWRKLLAYNLD 116
DB 56 SGIFVANVSSRPDCDALVAATVERFRIDTVNNAAGMNFVGTTOETSDQDWDCEIASDLS 115

QY 117 GVFFGTRGLGIQRMK-NKGLGASIISSIEGFVGDPSLGAYNASKGAVRIMSKSAALDCA 175
DB 116 GVFYMSRAAVPHLKETKG---SIVNIGSVSLGGLGSHAAAYNAKGGVANLTRSAA--CD 170

QY 176 LKDYDVVRVNTVHPGYIKTPLVDDLPGAEEAMSORT--KTPMGHIGEPNDIAYICVYLASN 233
DB 171 LGRFGVRANTVAPGLTVTGMVEAID--DDALLEKAWDRIPLRAGQP---ASAVAFVLSAD 226

QY 234 ESKFATGSEFVVDGGYT 250
DB 227 EAAWITGIVLPVDGGQT 243

Search completed: October 30, 2002, 15:46:02
Job time : 31 secs